

FIG.1A

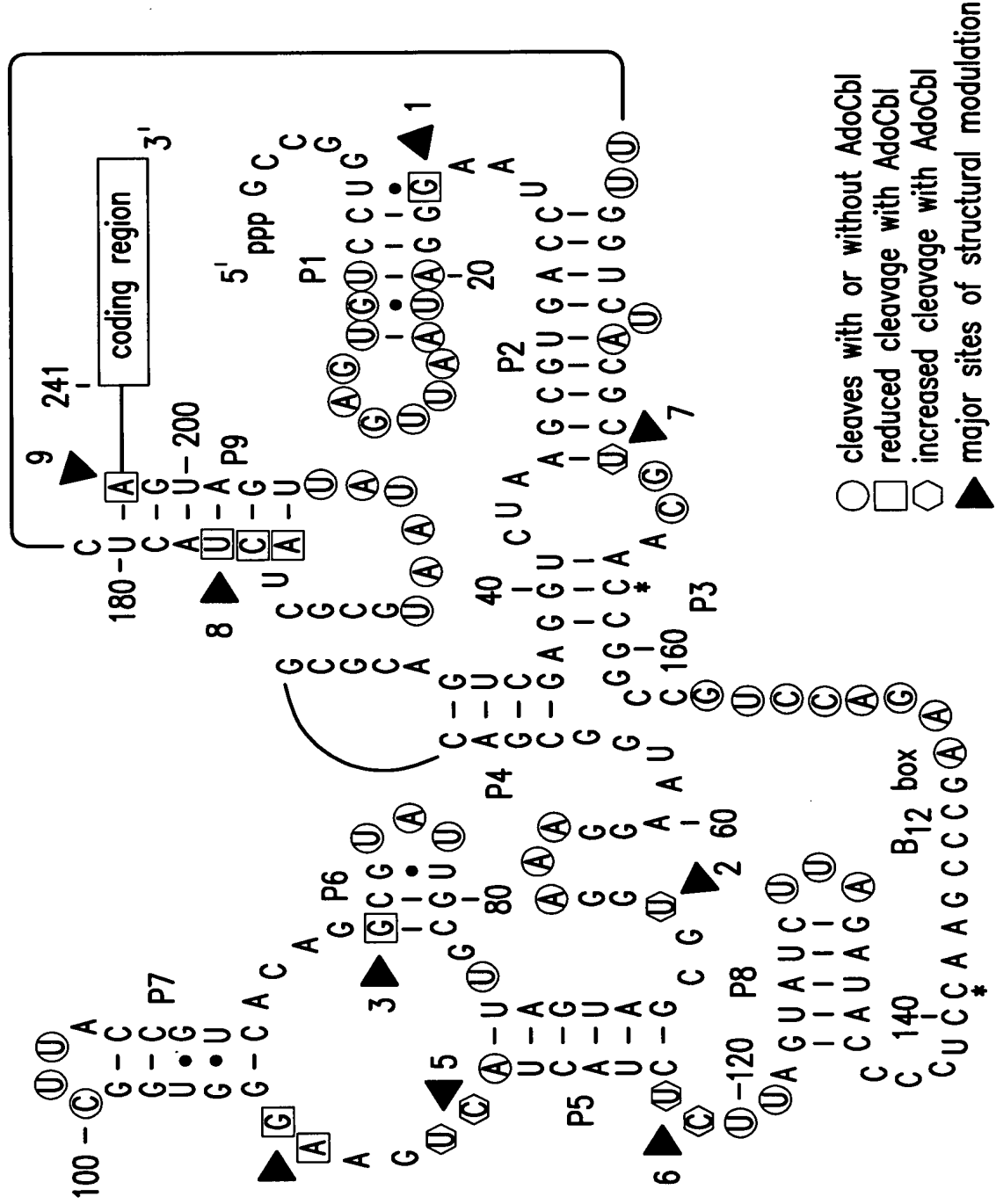


FIG.1B

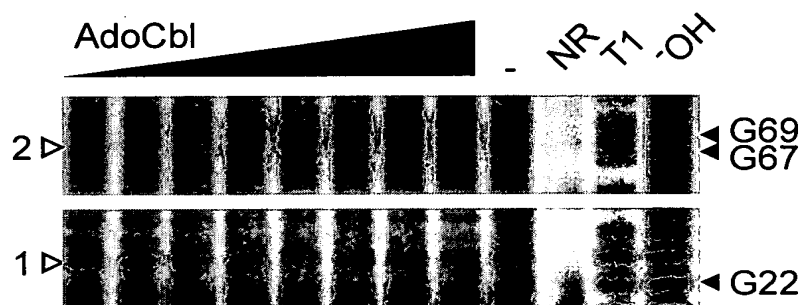


FIG.2A

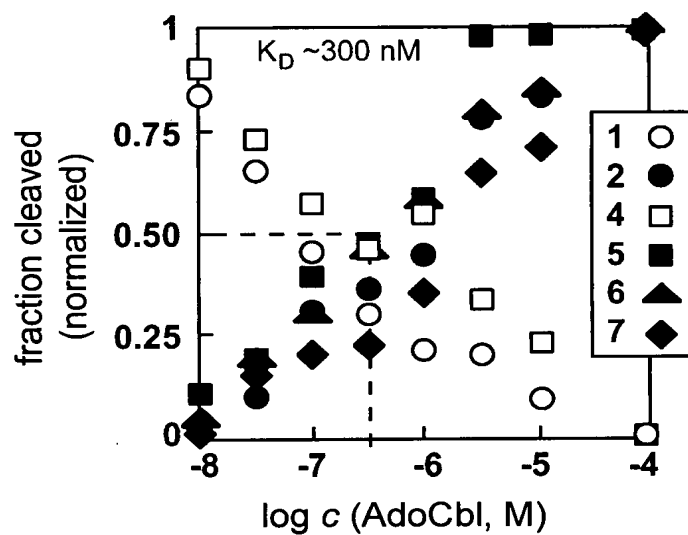


FIG.2B

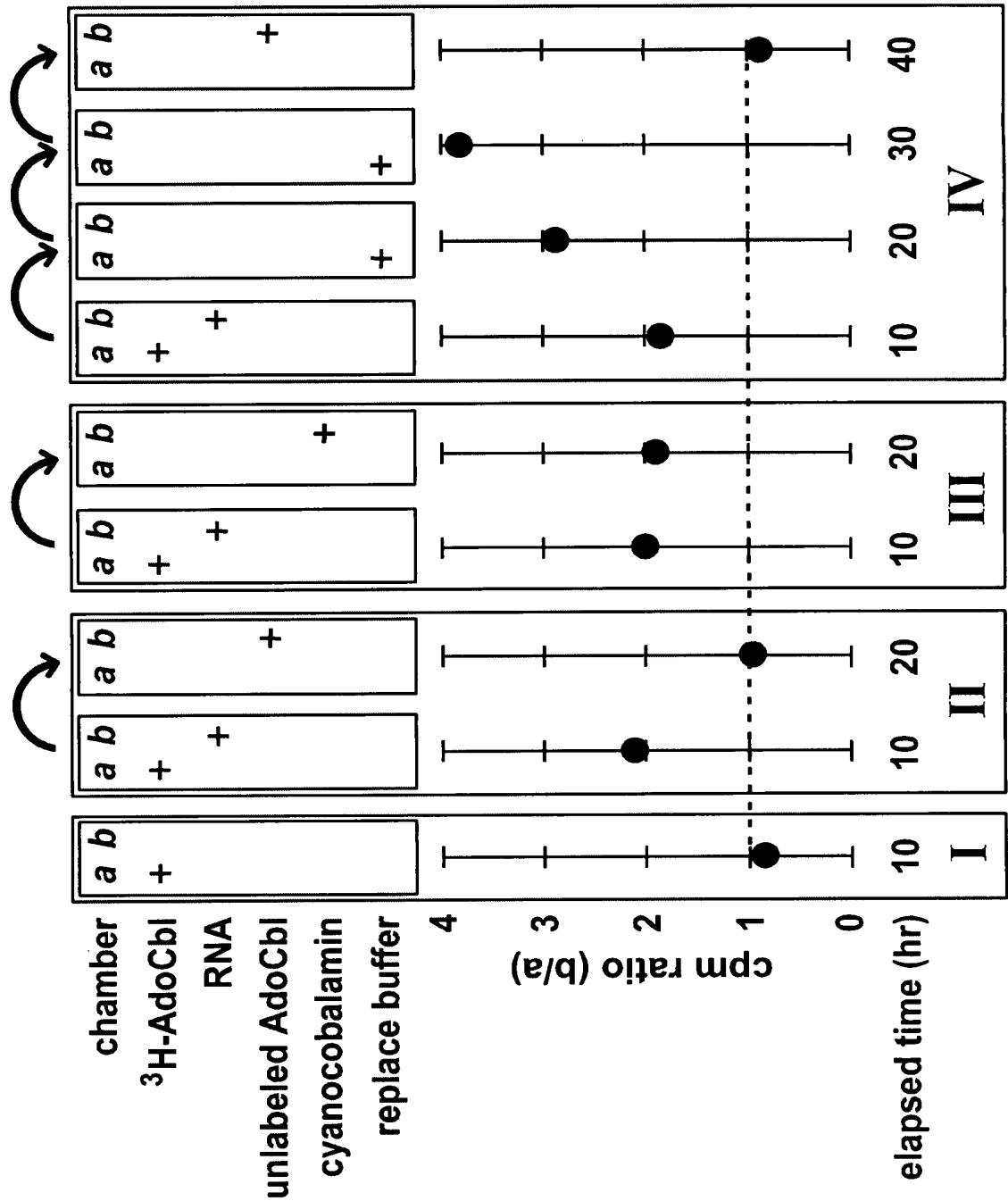


FIG.3

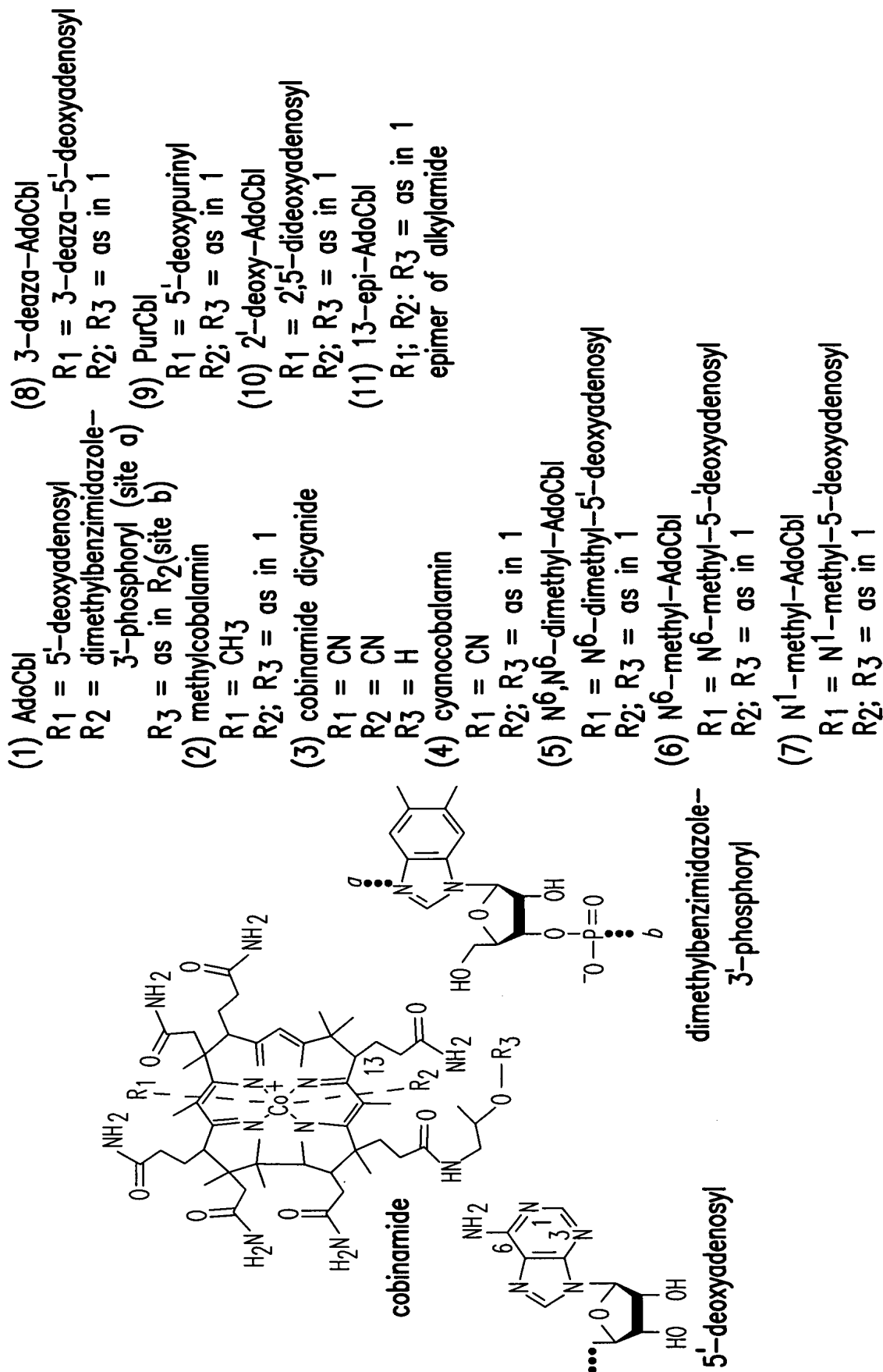


FIG. 4A

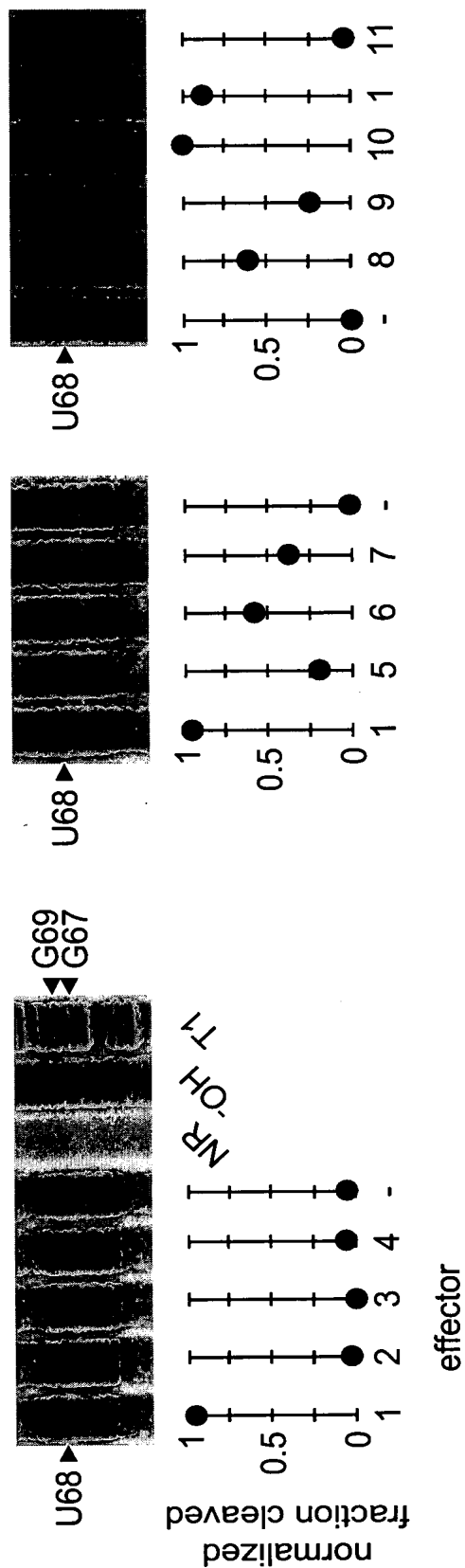


FIG. 4B

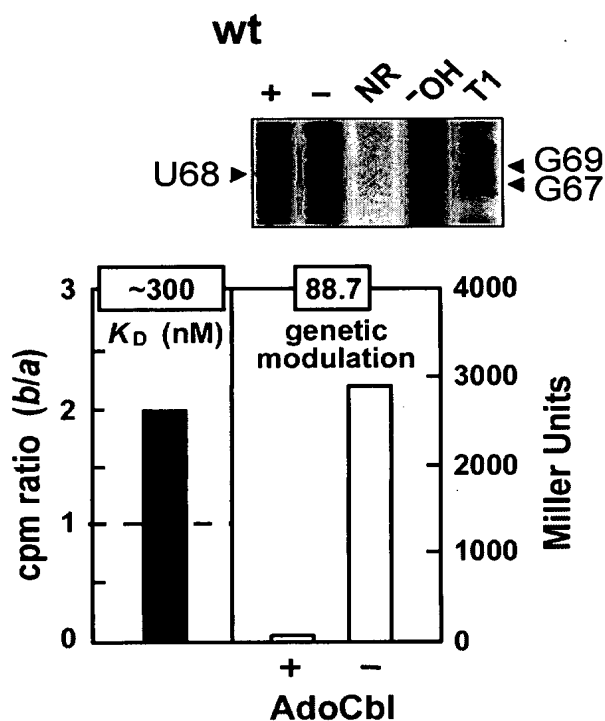


FIG.5A

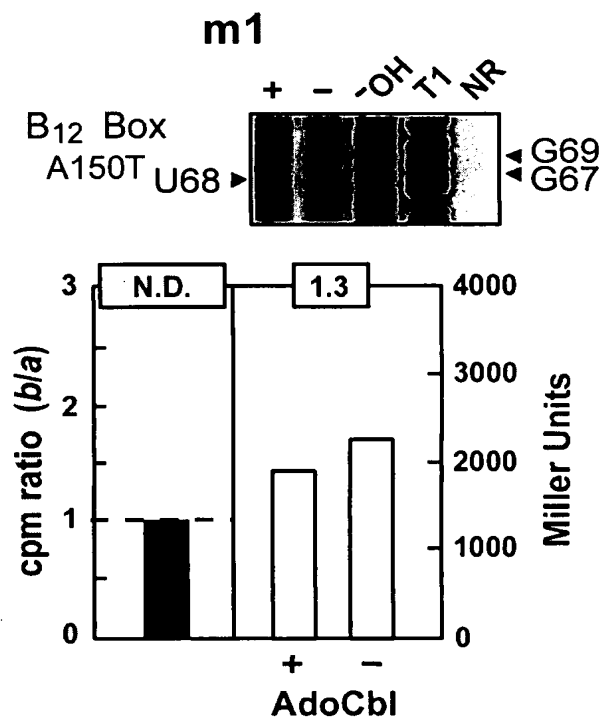


FIG.5B

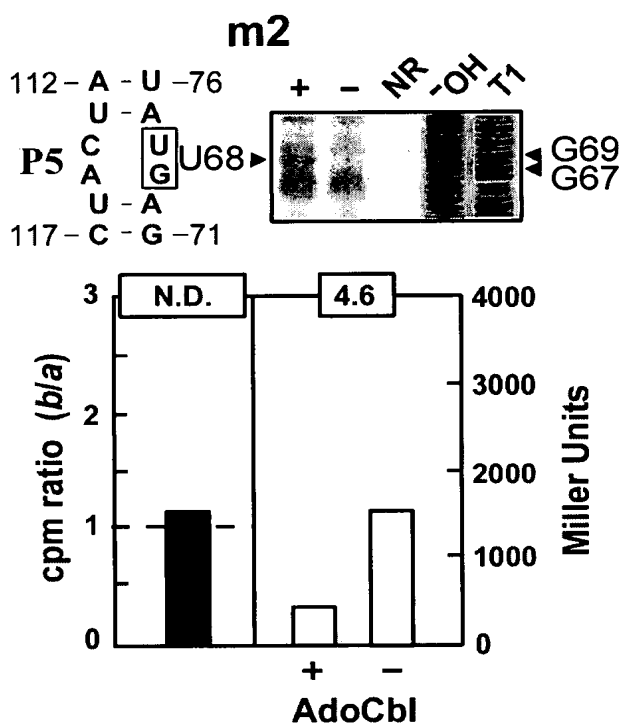


FIG.5C

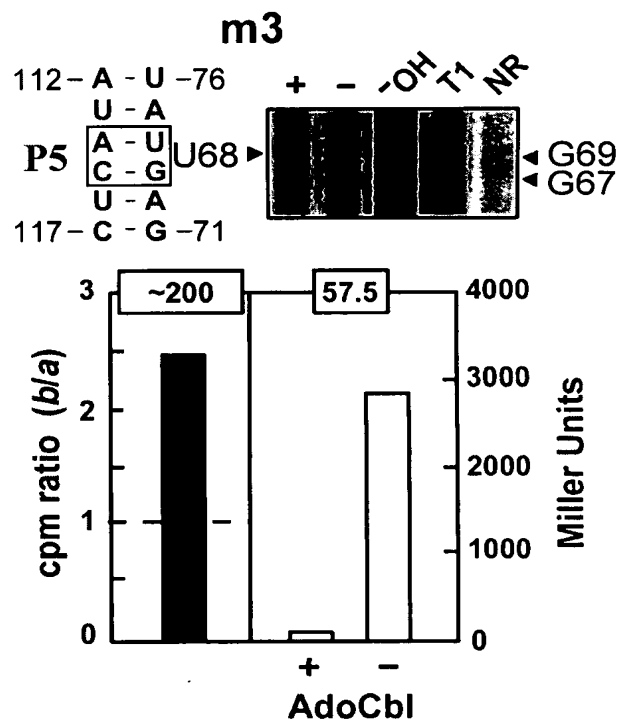


FIG.5D

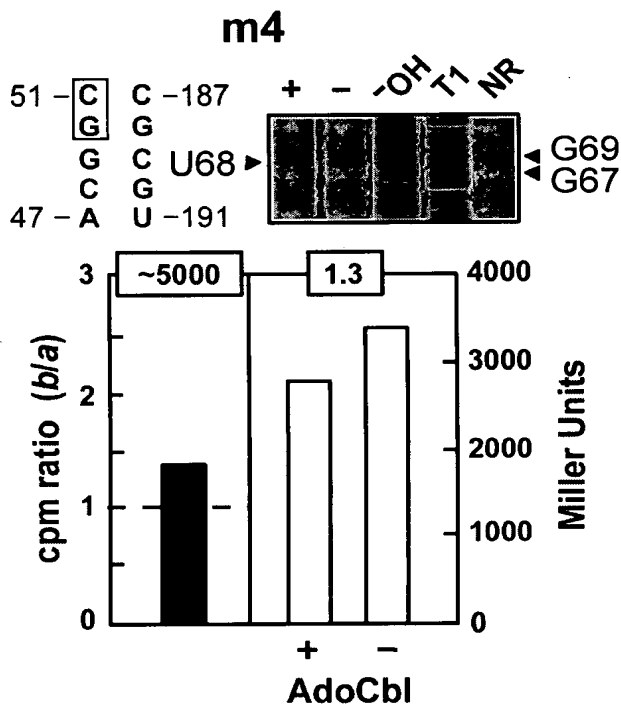


FIG.5E

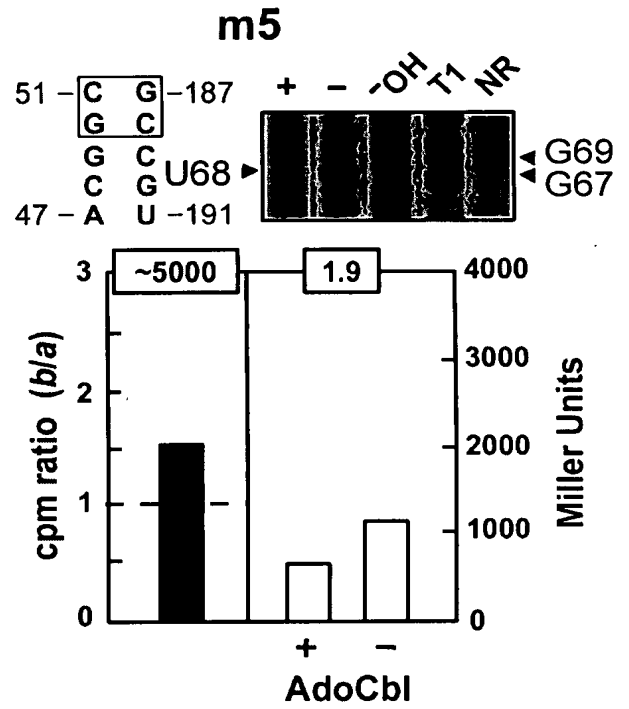


FIG.5F

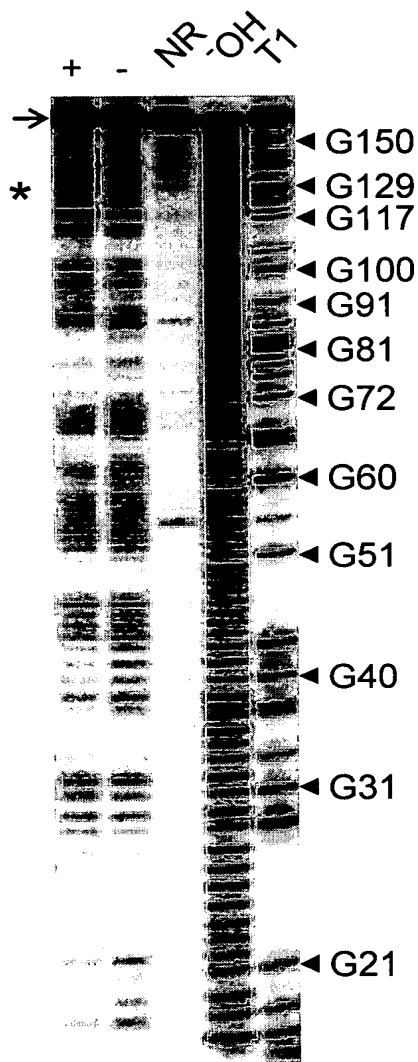


FIG. 6A

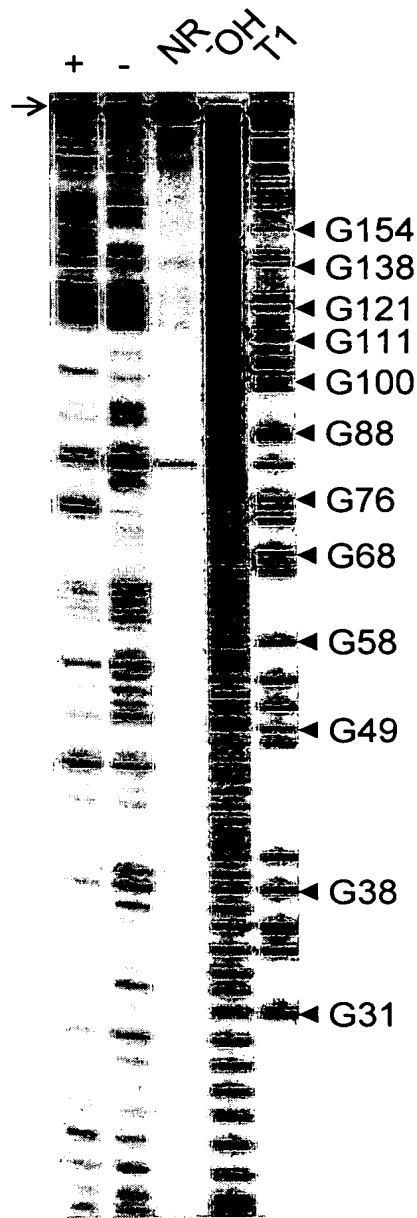


FIG. 6C

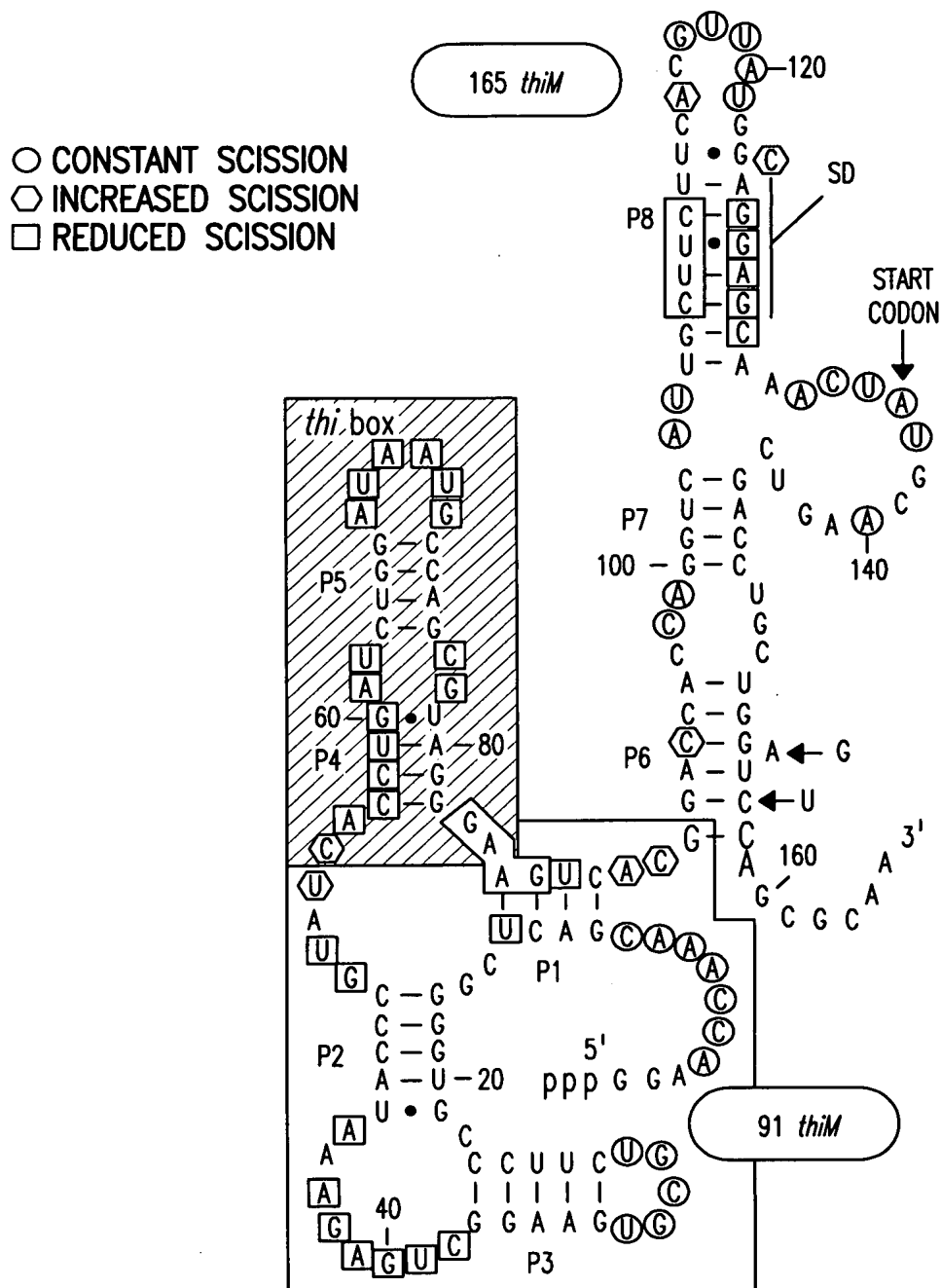


FIG.6B

- CONSTANT SCISSION
- ◊ INCREASED SCISSION
- REDUCED SCISSION

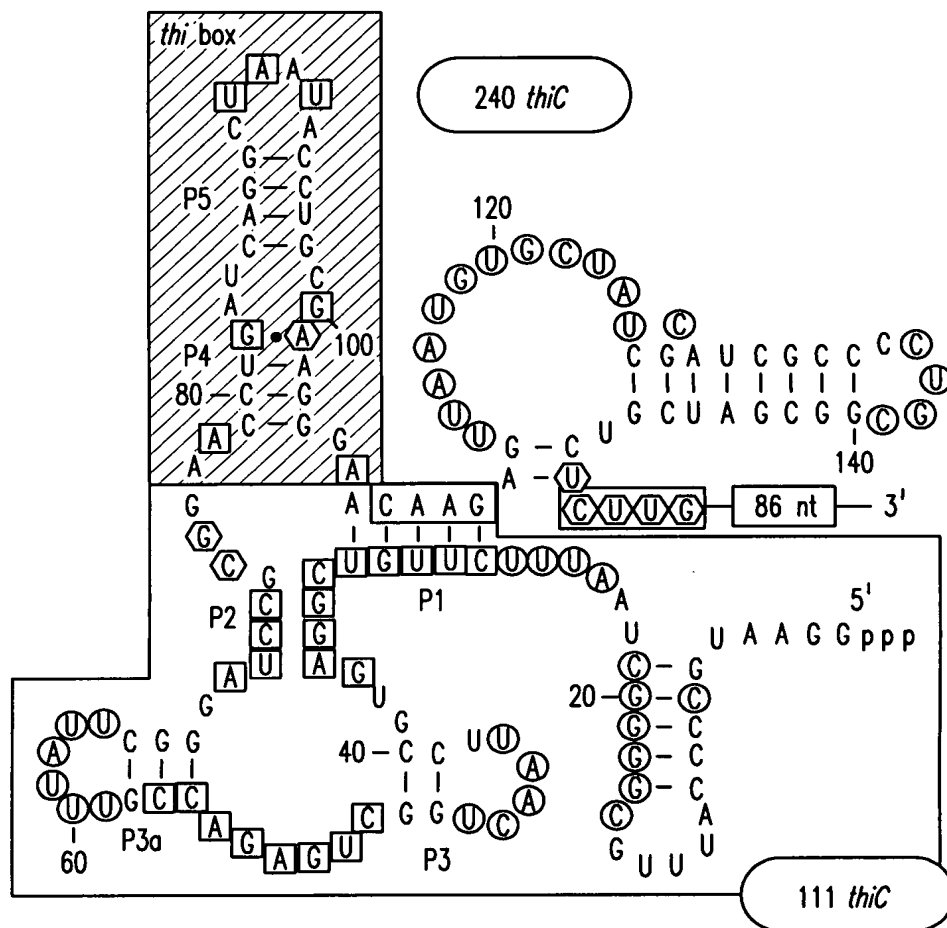


FIG.6D

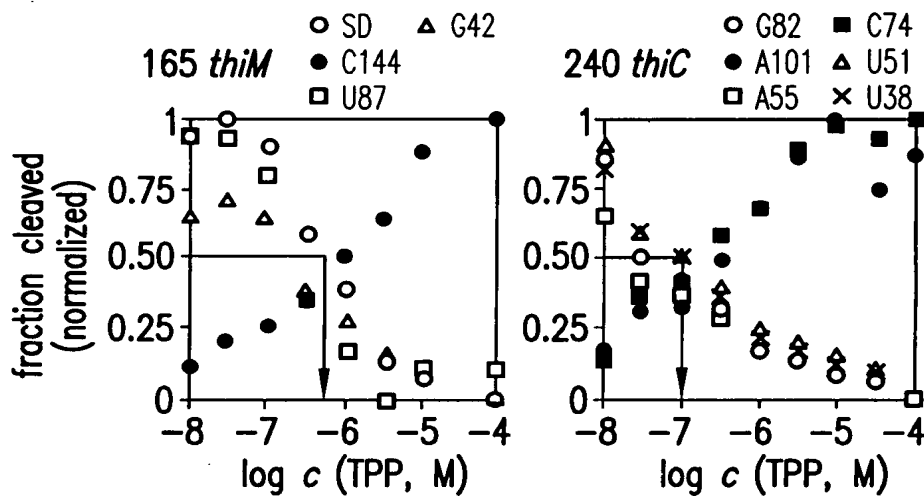


FIG. 7A

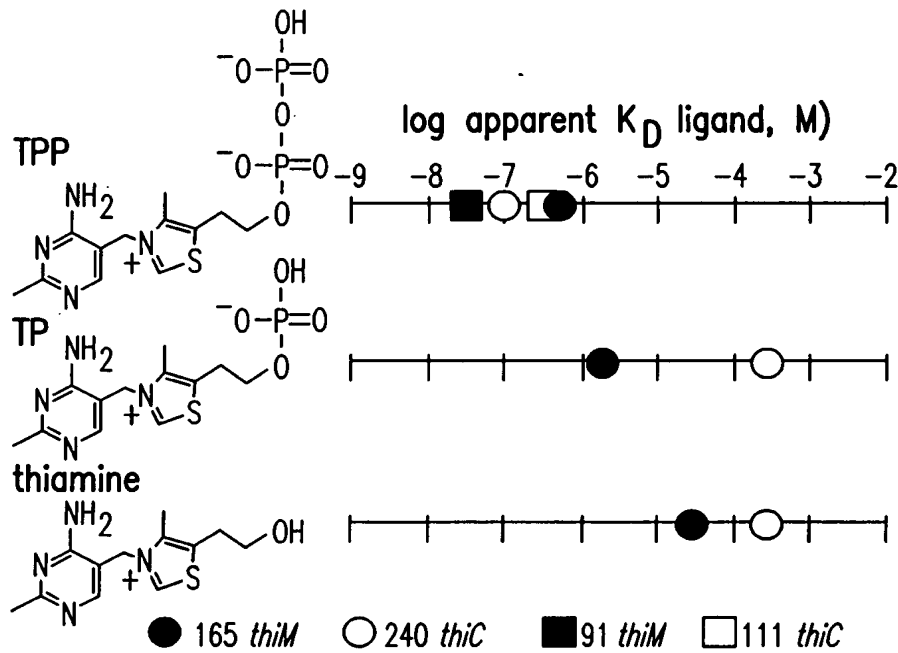


FIG. 7B

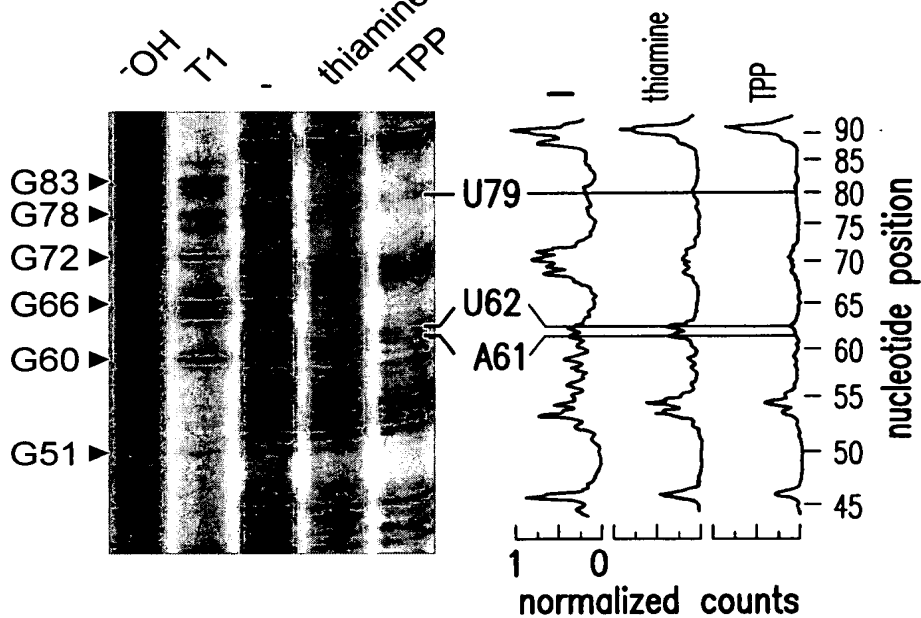


FIG. 7C

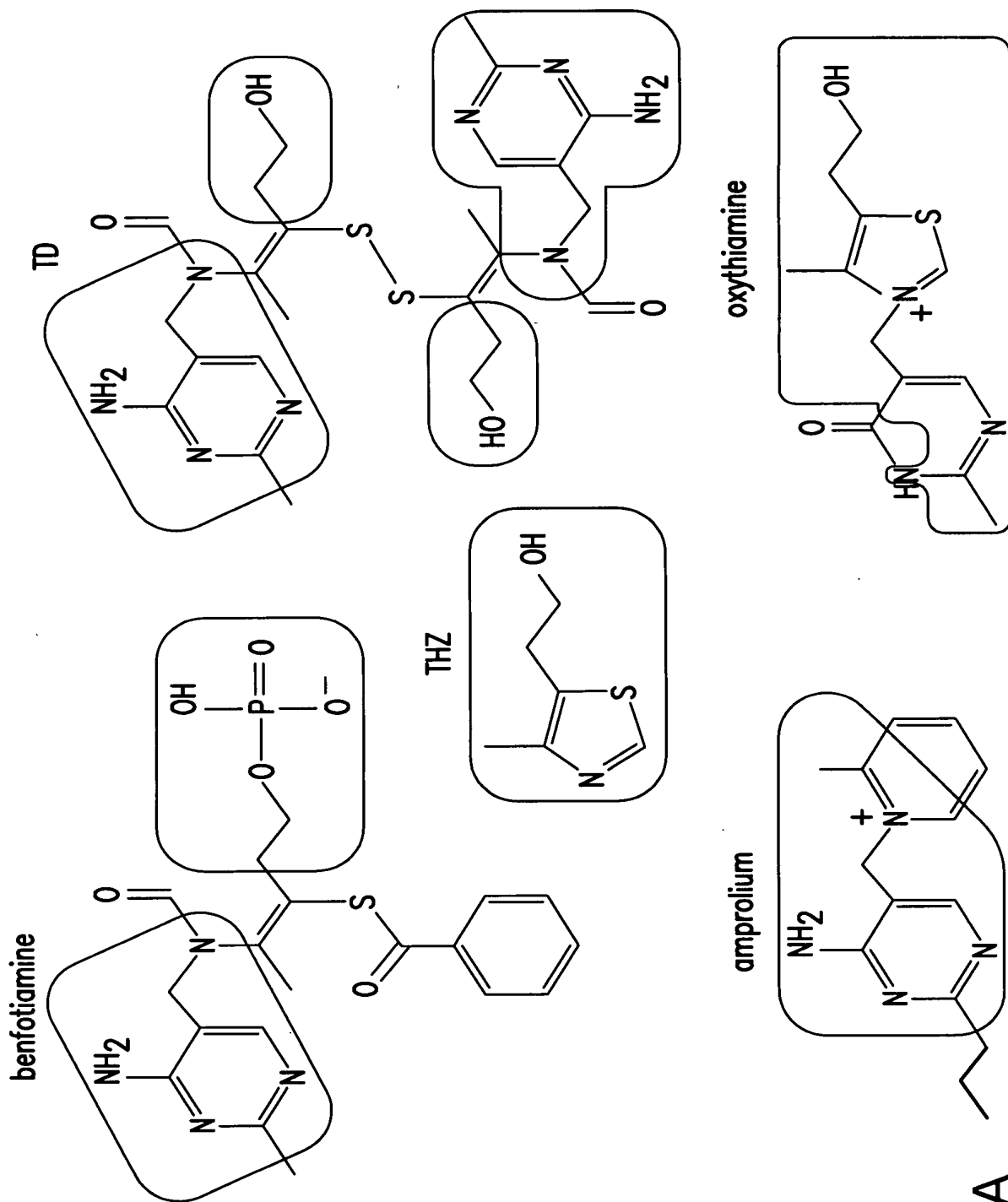


FIG. 8A

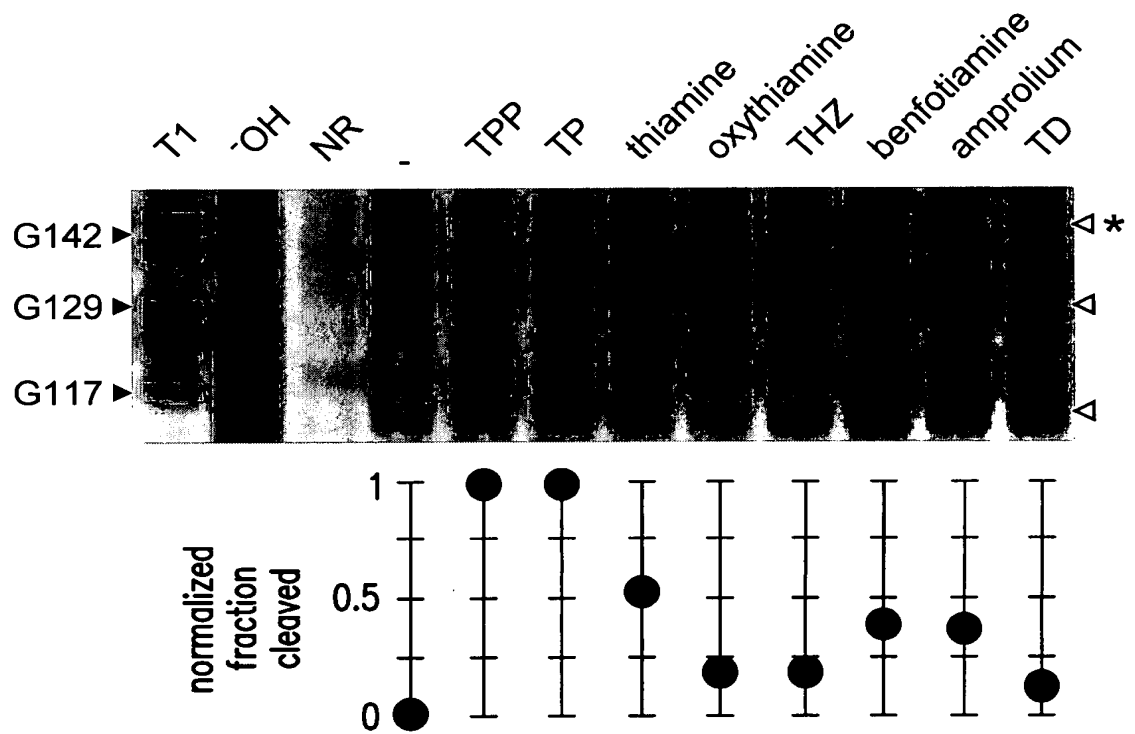


FIG.8B

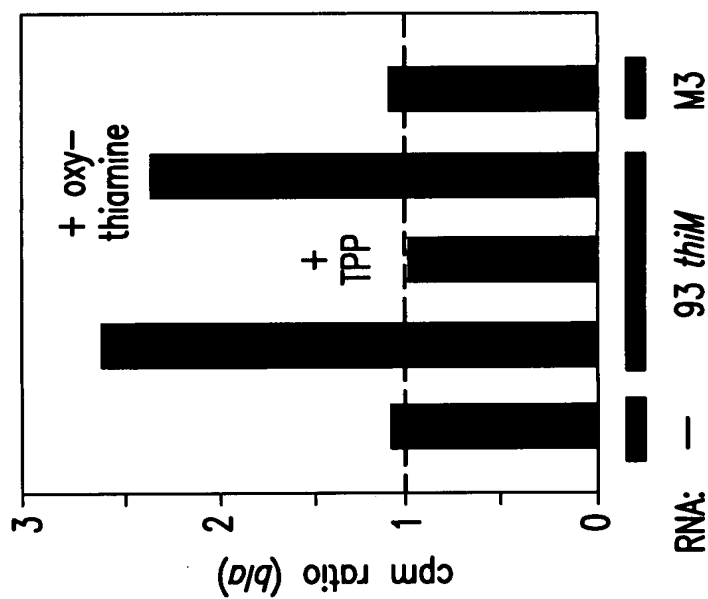


FIG.8D

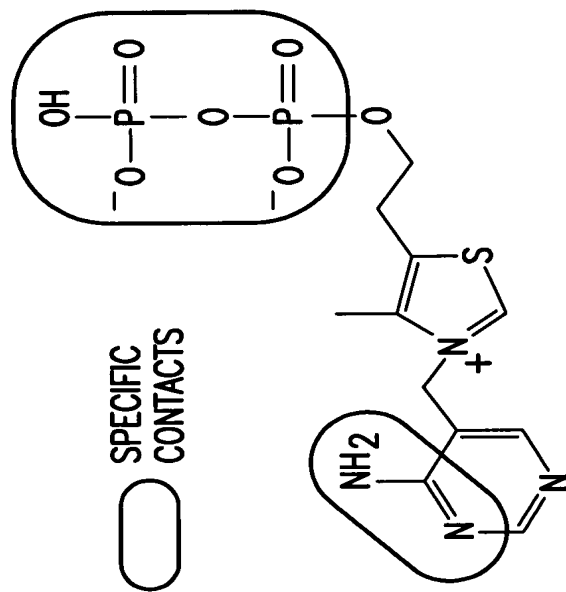


FIG.8C

SPECIFIC
CONTACTS

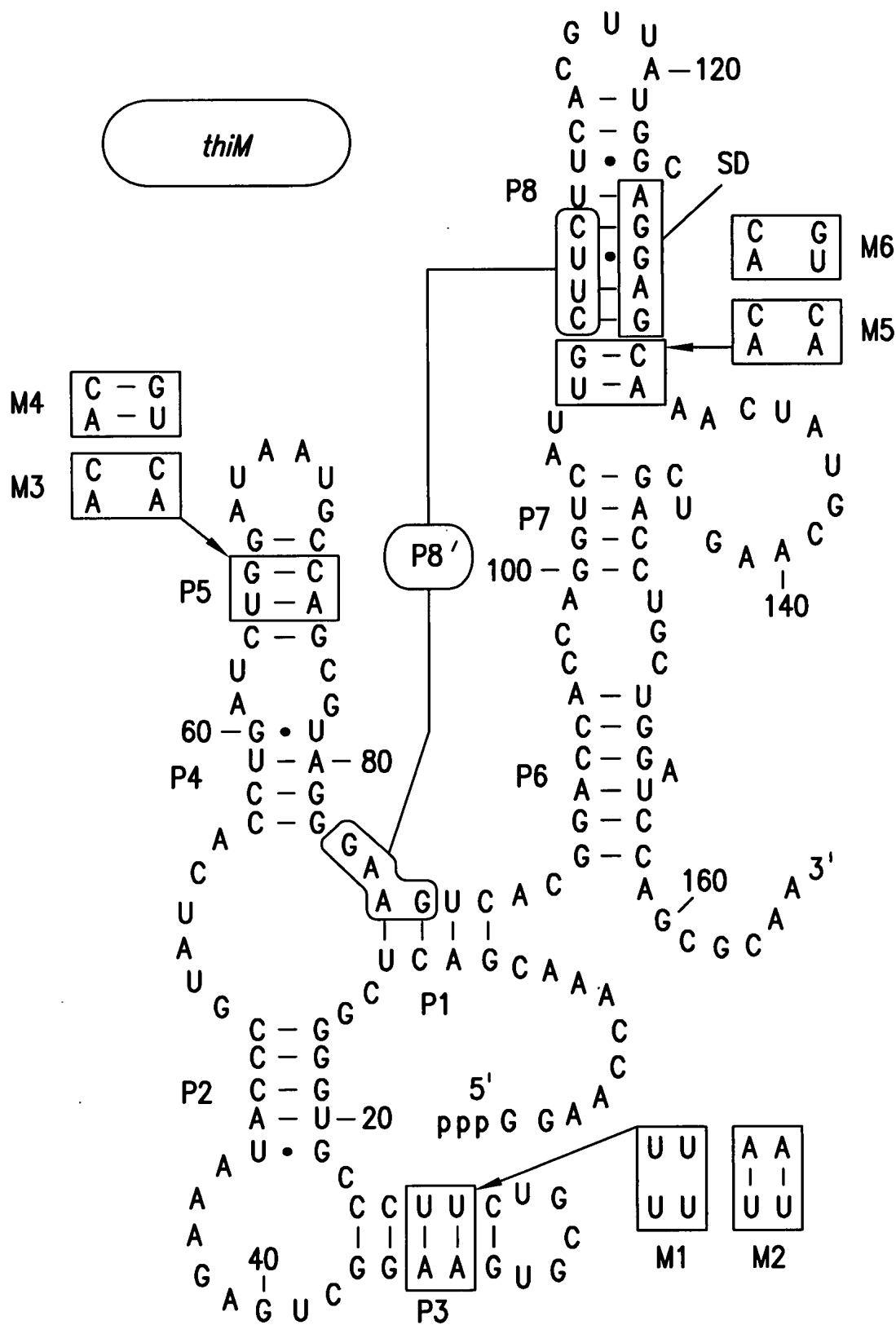


FIG.9A

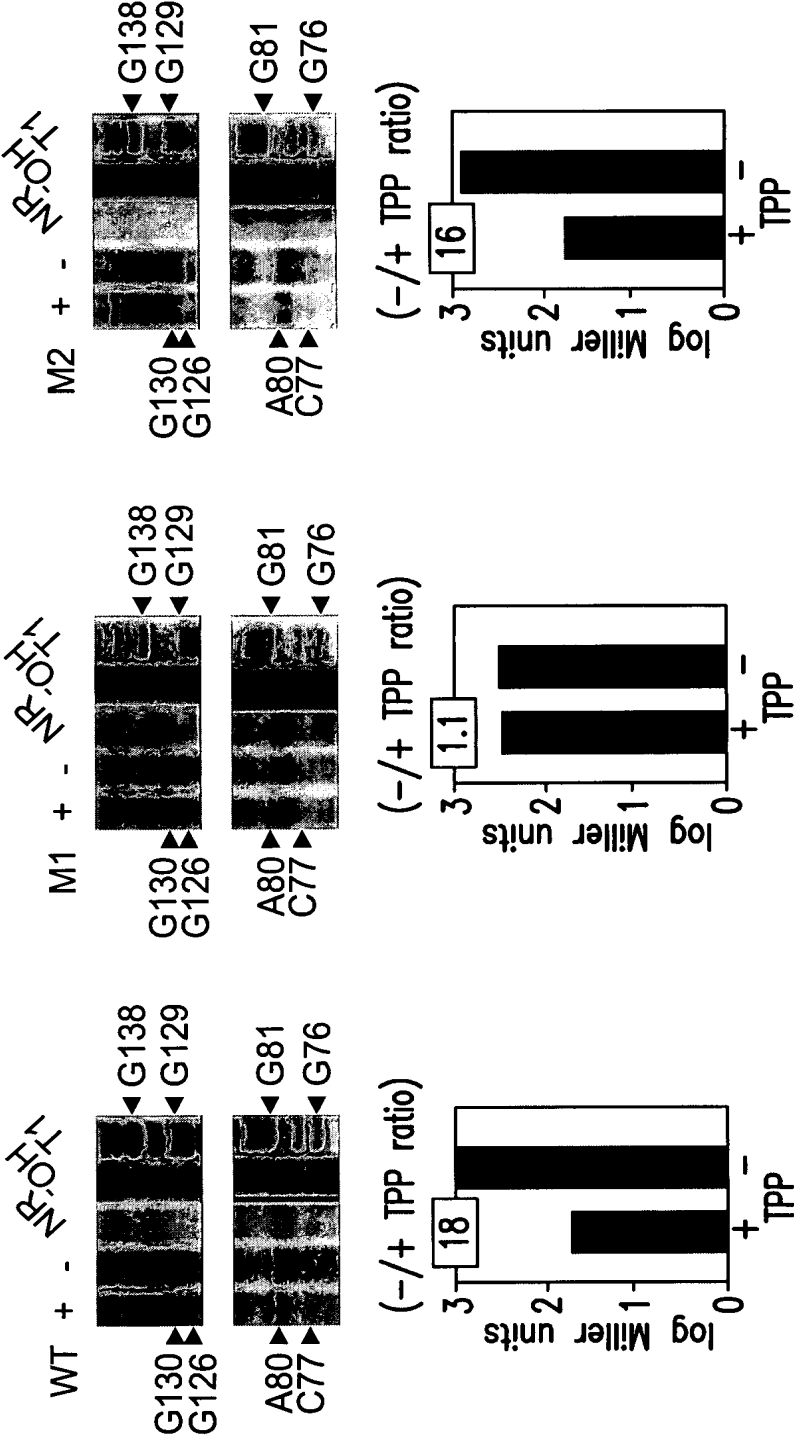


FIG.9B-1

mutant	TPP binding	SD status (+ TPP)	genetic modulation (-/+ TPP ratio)
WT	yes	closes	18
M1	no	unchanged	1.1
M2	yes	closes	16
M3	no	unchanged	1.1
M4	yes	closes	4.8
M5	no	unchanged	2.1
M6	yes	n.d.	10
M7	yes	n.d.	4.1
M8	yes	n.d.	1.6
M9	yes	n.d.	2.4

FIG.9B-2

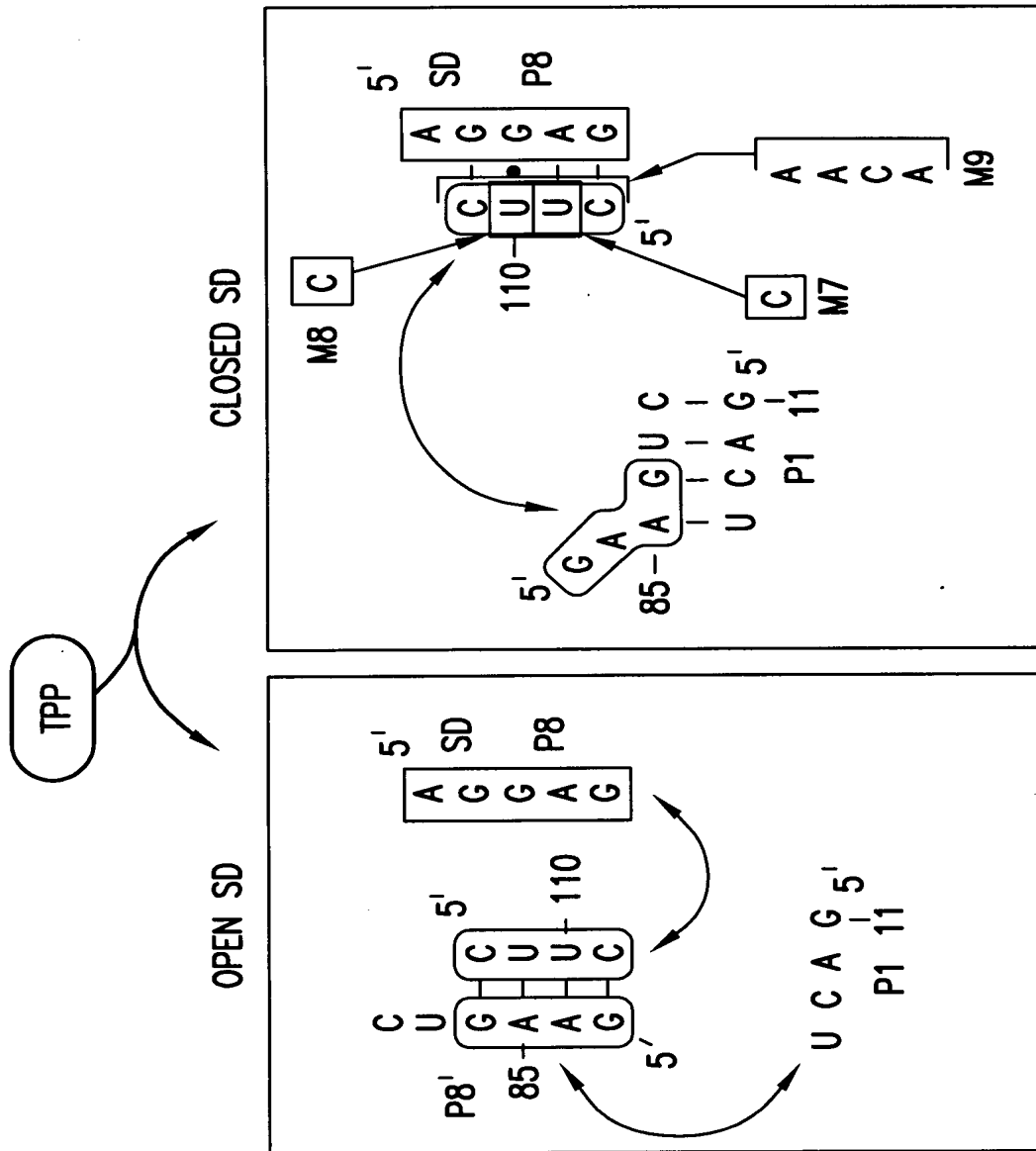


FIG.9C

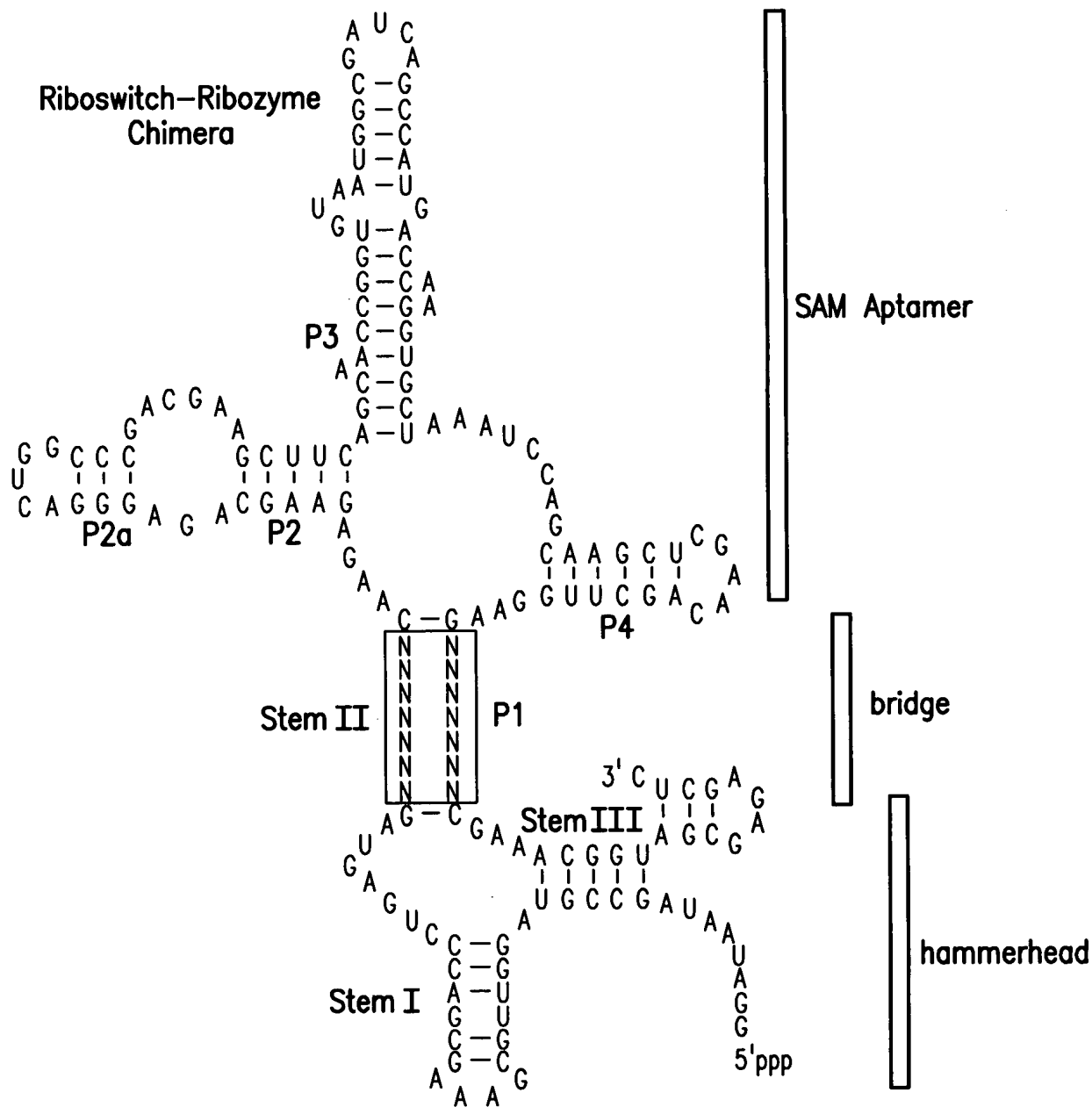


FIG.10

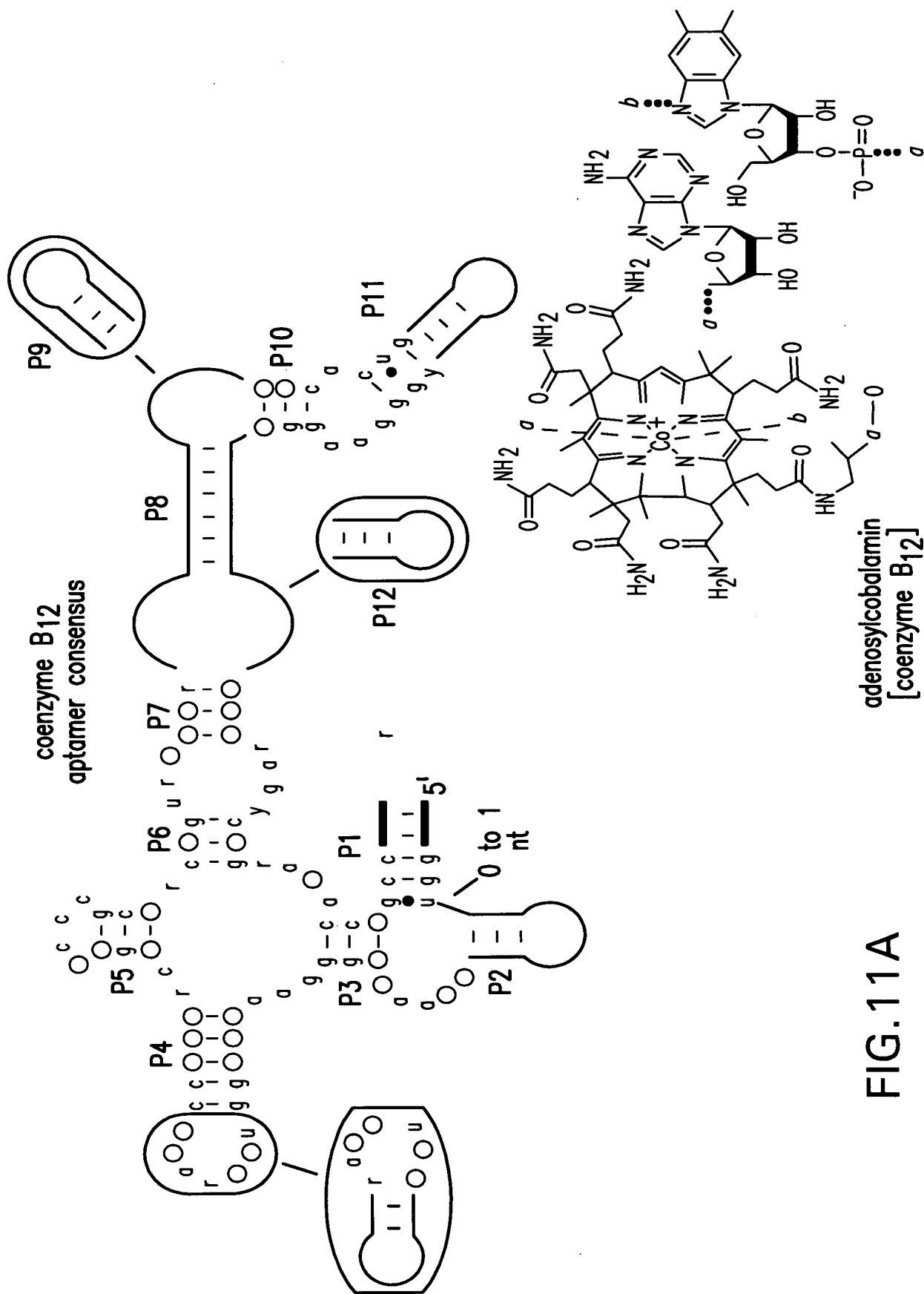


FIG. 11A

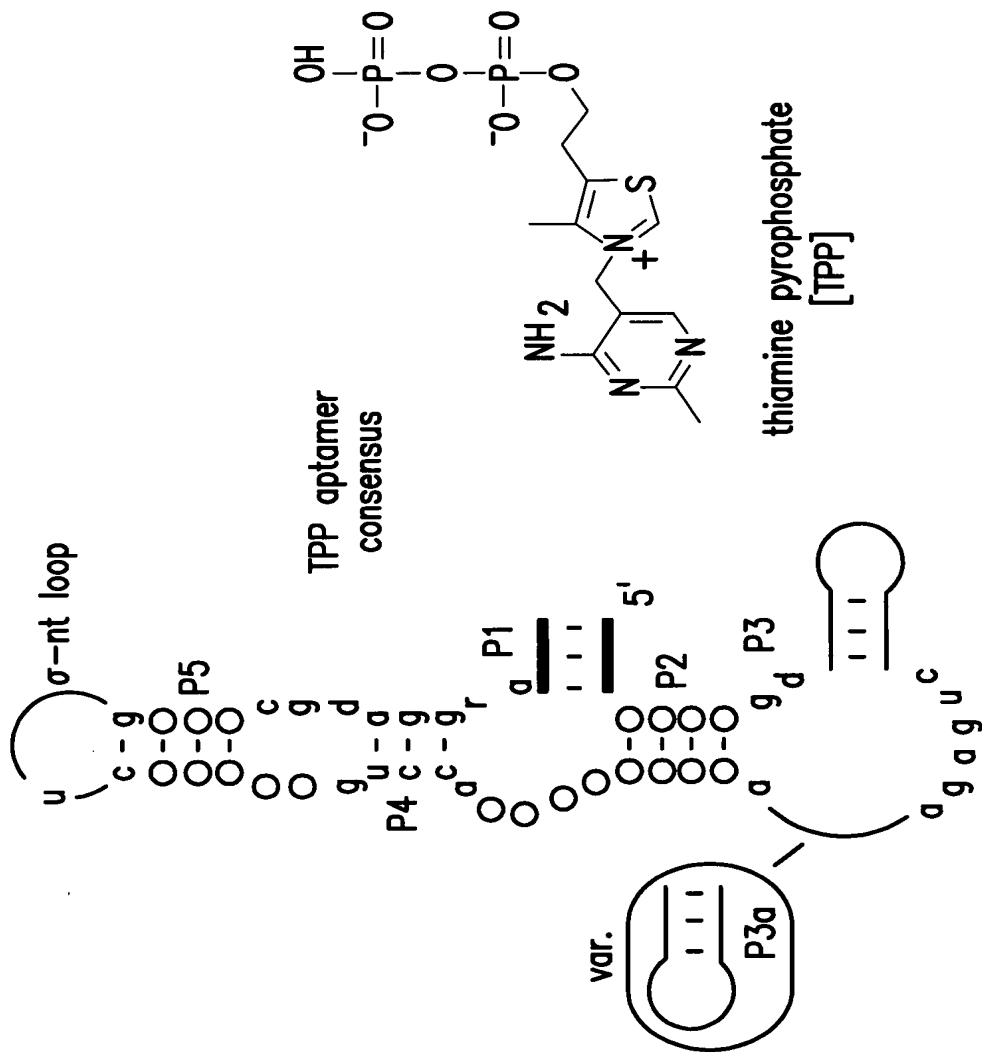


FIG. 11B

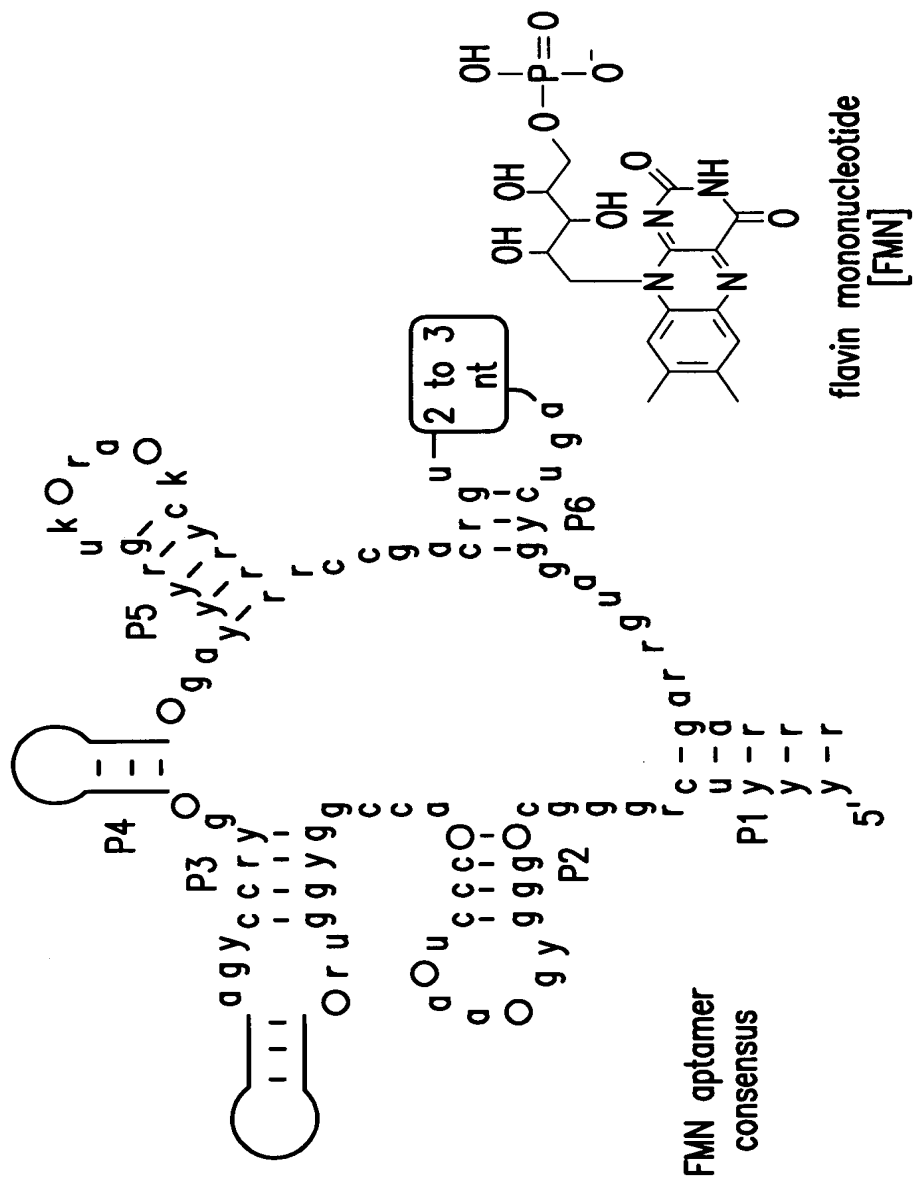


FIG. 11C

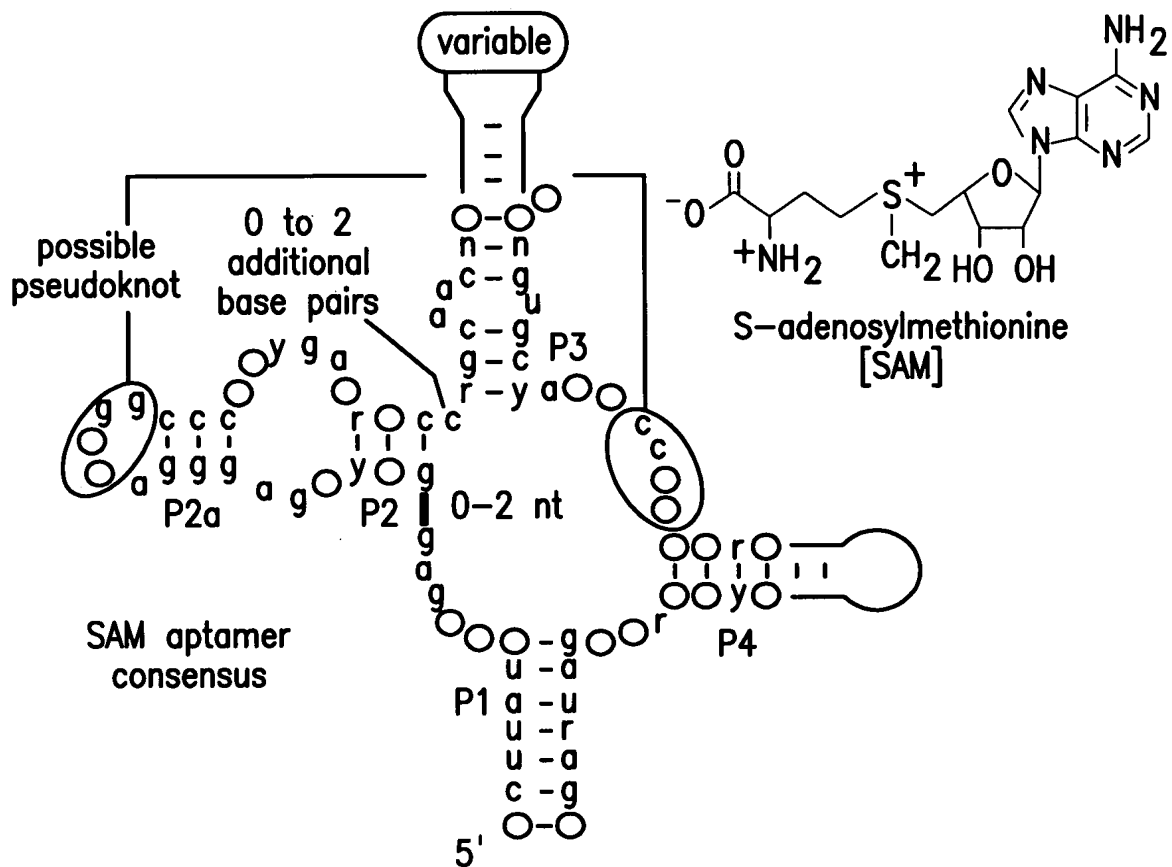


FIG. 11D

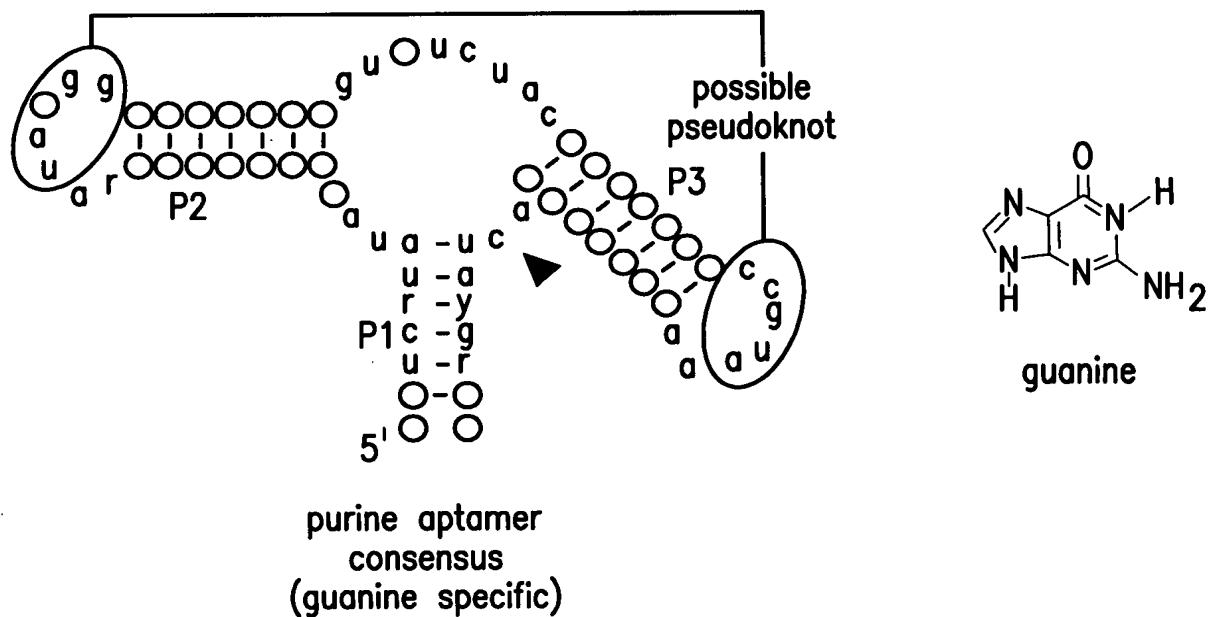


FIG. 11E

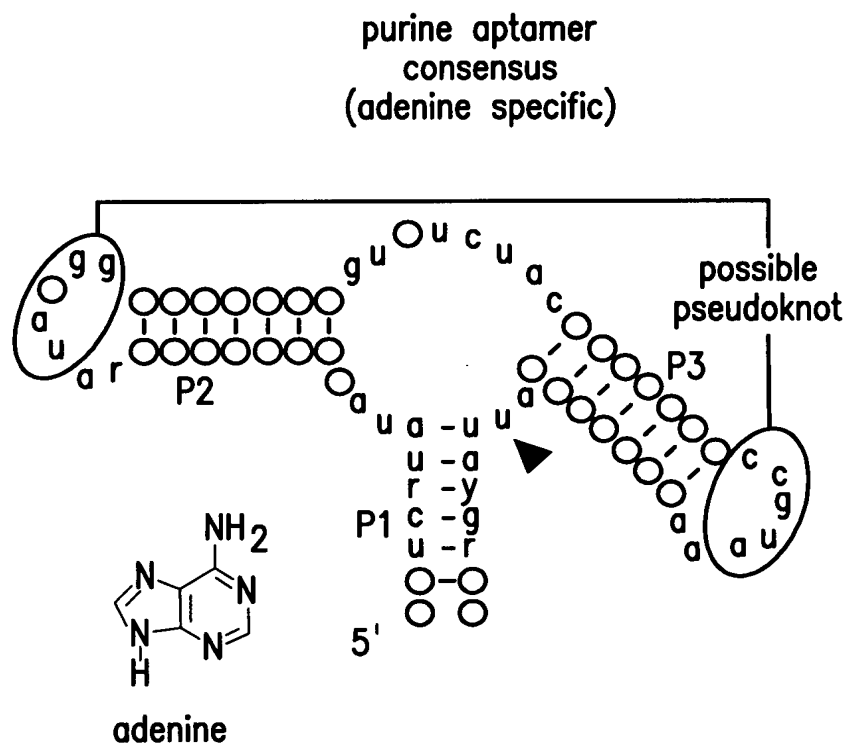


FIG. 11F

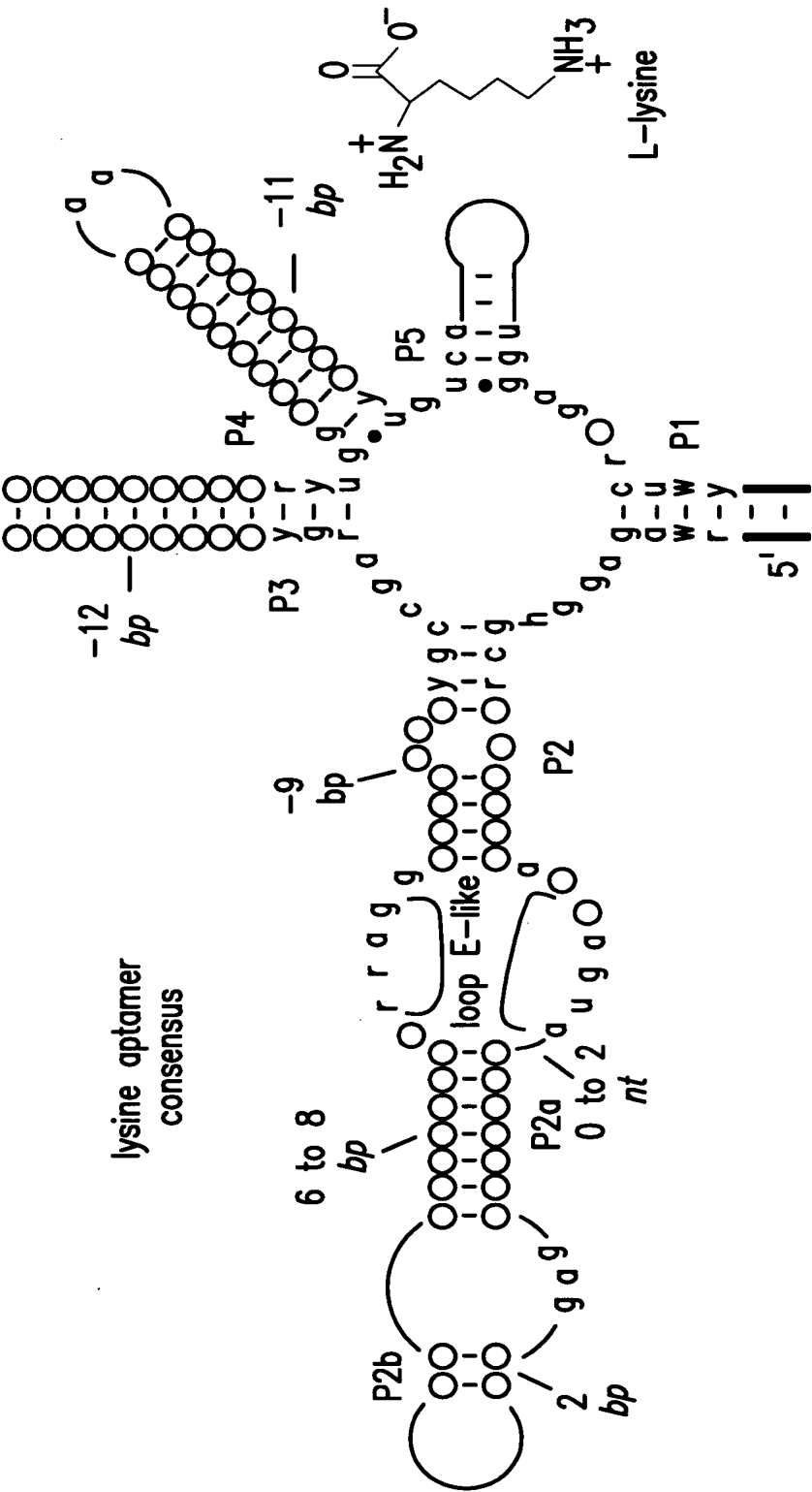


FIG.11G

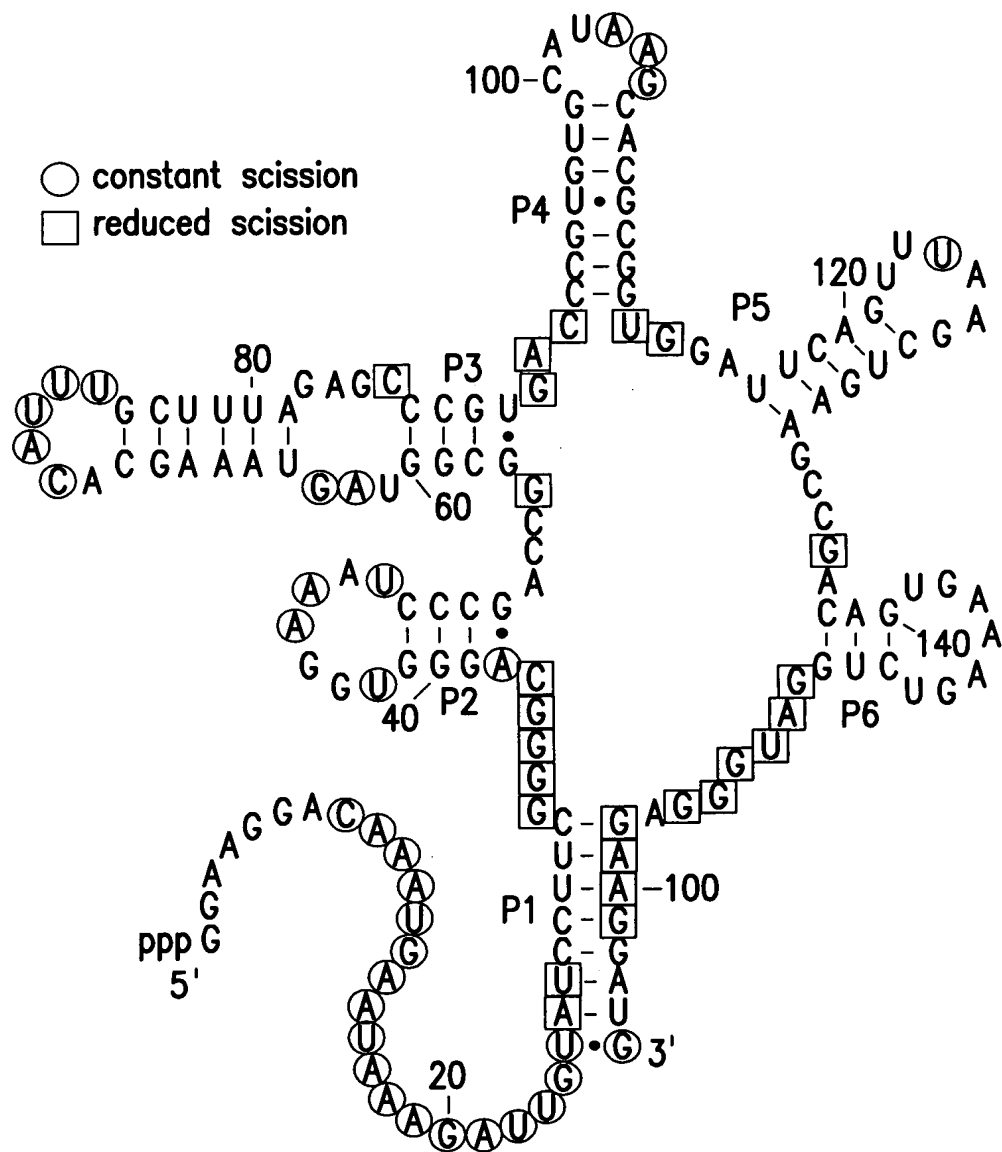


FIG. 12A

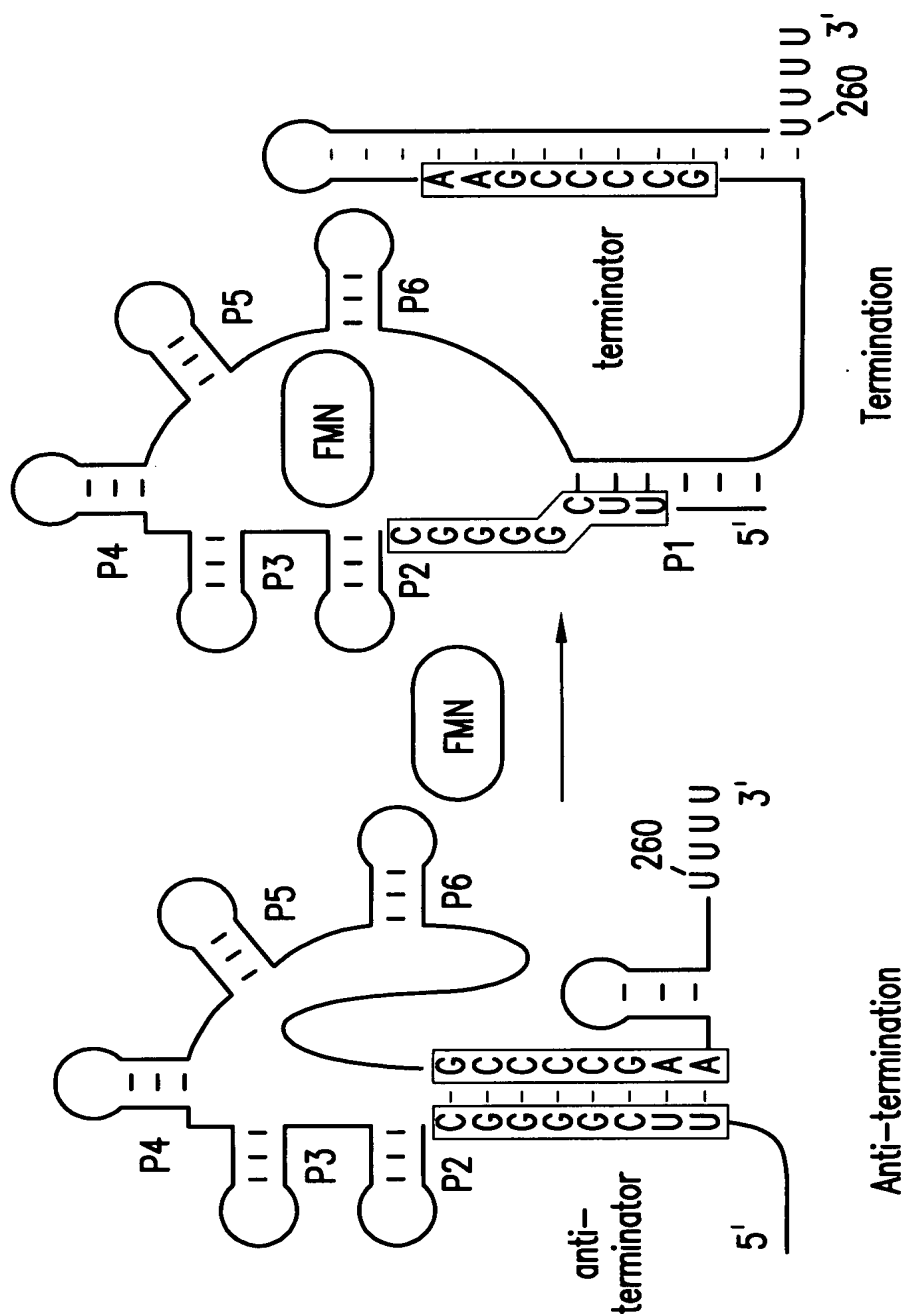
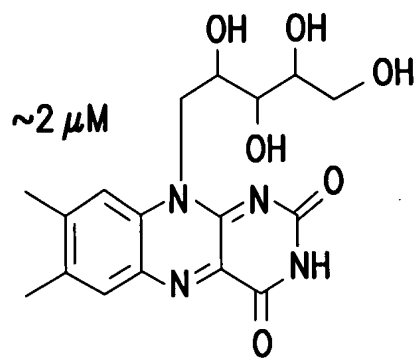
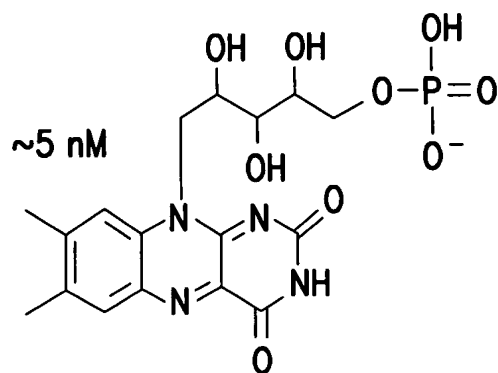


FIG. 12B



riboflavin



FMN

FIG. 12C

[illegible]

FIG. 13B

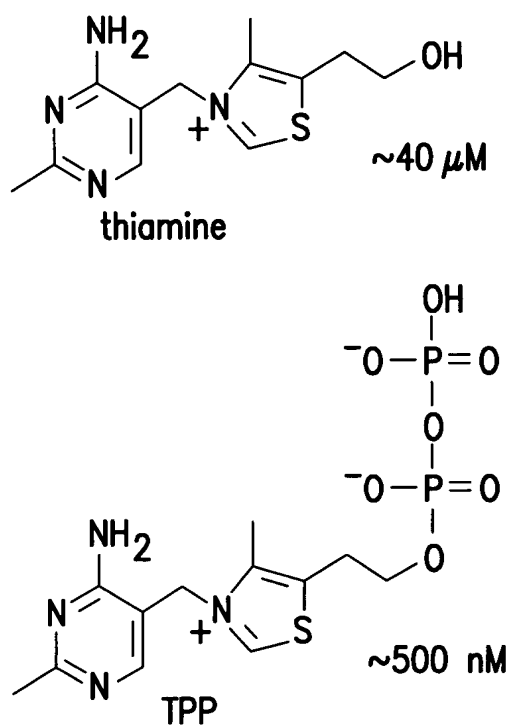


FIG.13C

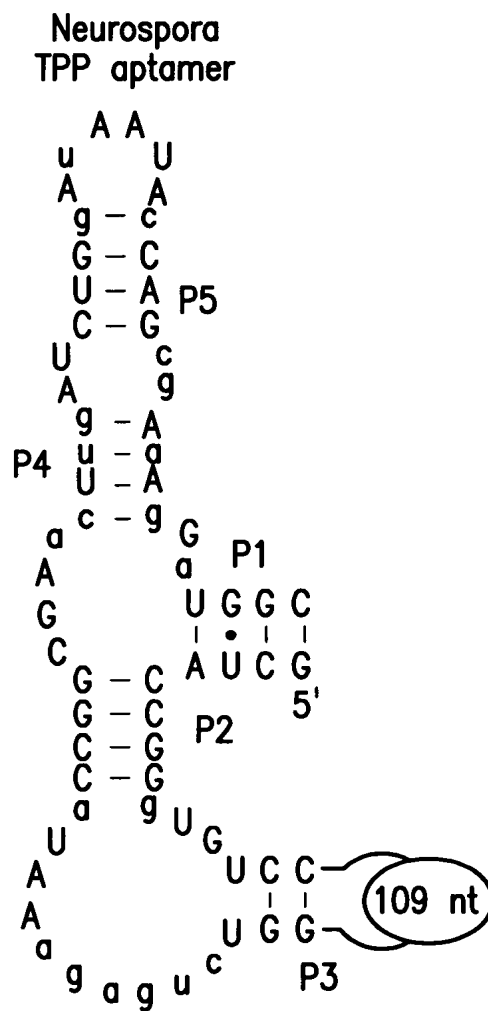


FIG.14C

ID	Position	Accession	Sequence Name	Gene	Location
Eco1	-	2183373	NC_000913.1 Escherichia coli K12 complete genome	thiM operon	5'UTR
Eco2	-	4193775	NC_000913.1 Escherichia coli K12 complete genome	thiC operon	5'UTR
Cac	-	3156135	NC_003030.1 Clostridium acetobutylicum ATCC824 complete genome	thiC	5'UTR
Ncr	+	664	AY007661.1 Neurospora crassa thiamine biosynthesis protein nmt-1 gene	nmt-1	5'UTR
Aor	+	622	AF217503.1 Aspergillus oryzae putative thiazole synthase (thiA) gene	thiA [thi4]	5'UTR Intron
Fox	+	2156	AB033416.1 Fusarium oxysporum sti35 gene for stress-responsive gene product	sti35 [thi4]	5'UTR Intron
Fso	+	461	M33642.1 Fusarium solani ST135 protein gene	sti35 [thi4]	5'UTR Intron
Ath	-	78516	AC005496.3 Arabidopsis thaliana chromosome 2 clone T27A16 map mi54	thiamine gene [thiC]	3'UTR
Pse	+	2296	AF264021.1 Poa secunda putative thiamine biosynthesis protein ThiC mRNA	putative thiC	3'UTR
Osa	-	91318	AC084406.7 Oryza sativa chromosome 3 BAC OSJN Ba0067E01 genomic sequence	putative thiC	3'UTR

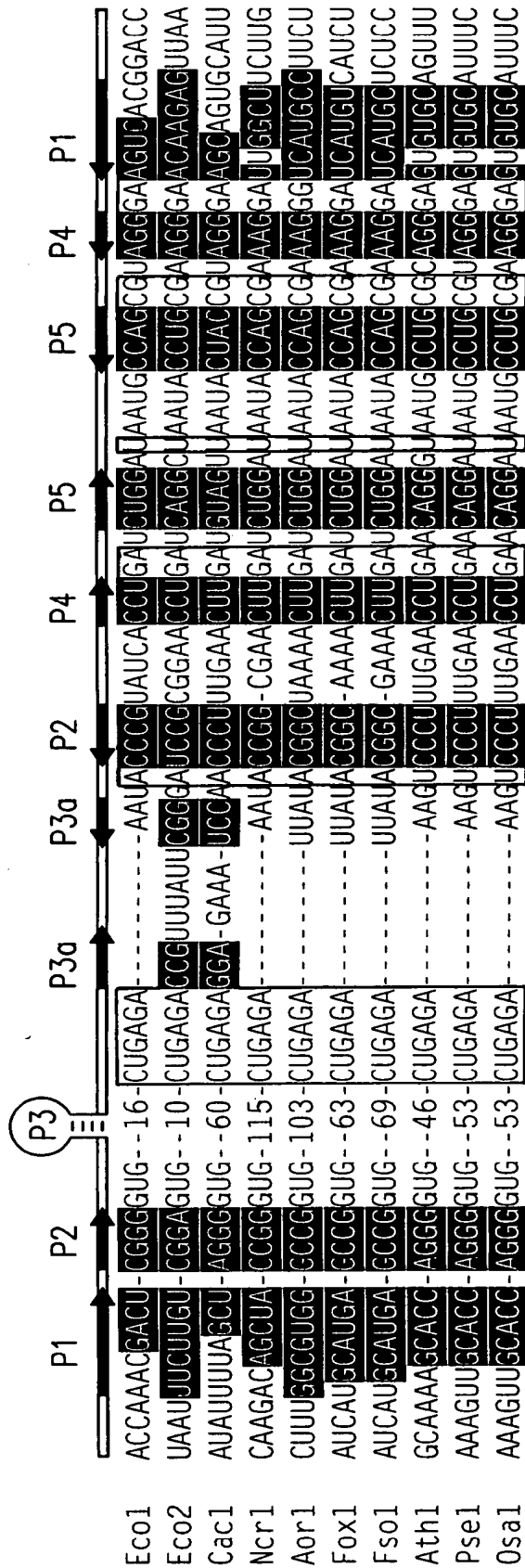


FIG.15

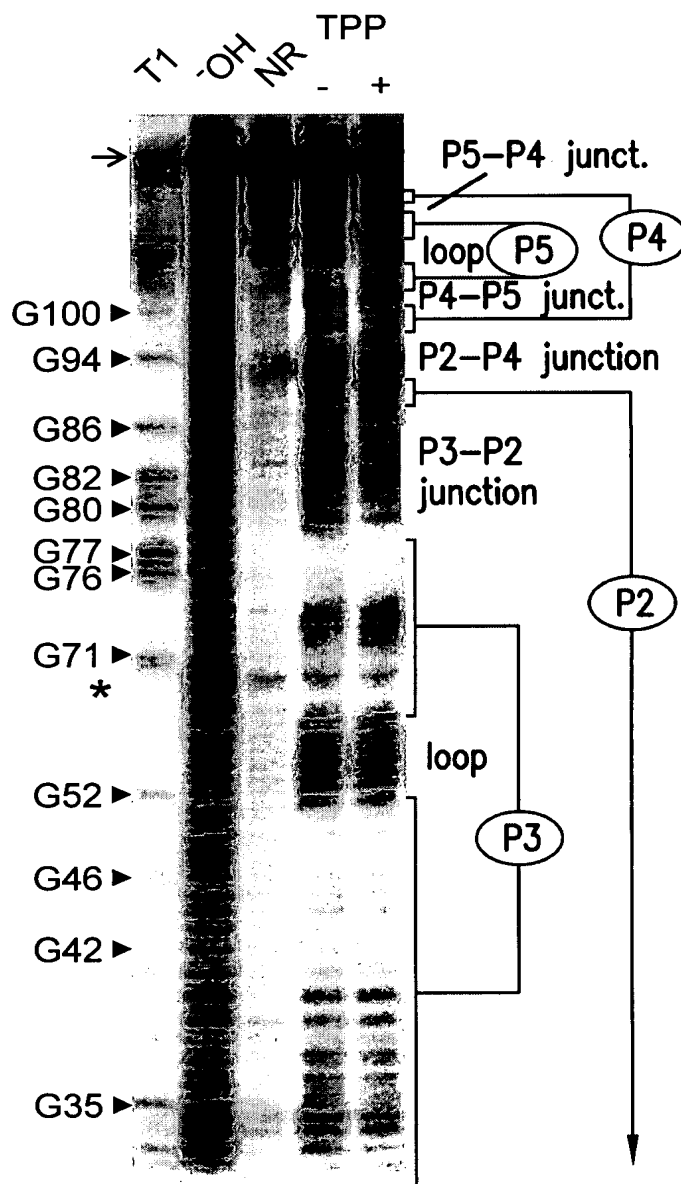


FIG.16A

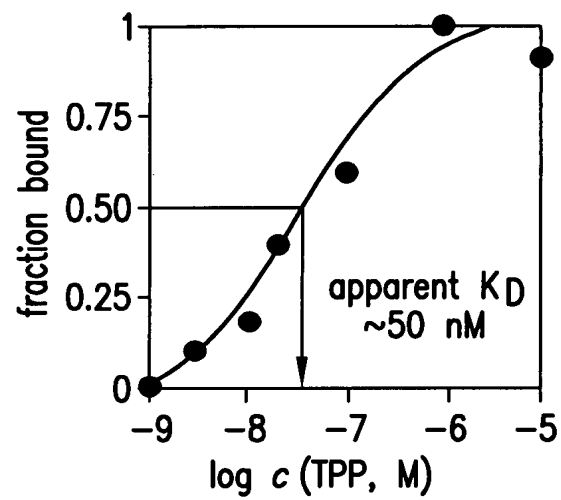


FIG.16B

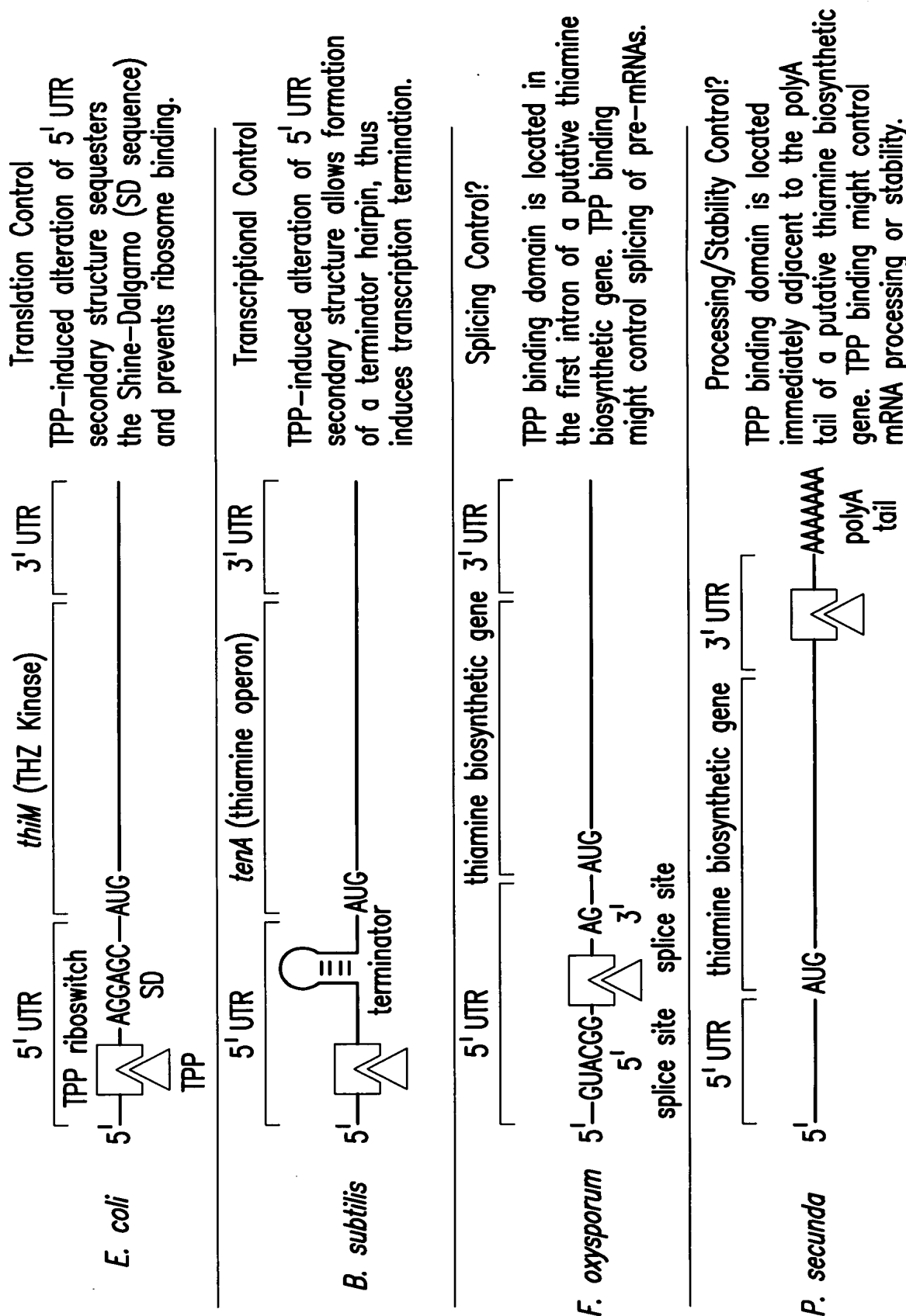


FIG. 17

	P1	P2	P2'
1	BA DBA5 CGGUGAGGUGagggUgcAGUCAUU--aAG--agua--UCAUUCUG--g--ag--AUAGUC--ALBAUGA--AGGAUGA--GaaaggAAUGAU--Ugcga		
2	BA IysA CUCAAGGUGagggCCgcGAUAGG--aAAGagua--AGCUAUGG--g--ag--UUAUUC--AA--GGUU--GaaaggGACUUAU--Ugcga		
3	BA IysP CGAUGAGGUGagggUgcGACUUAU--aAG--agua--AAAGCGAC--g--agAACGAGAA--GUCUAAGA--UCCGUUU--GaaaggAAAGU--Ugcga		
4	BH dapa AGUCAGGAUagggUgcAAAAACC--aAG--agua--CACAAU--Gg--ag--GAGAUGAGA--UCCGUUGAGAUUUG--GaaaggGGAA--UUUgcga		
5	BH IysC AGUGAGGUGagggUgcGAAACC--aAG--aguaC--ACAGUC--UCAG--ag--AAUGAGAUUCUUC--GACUUUGGaaaggGGGA--UUCgcca		
6	BH nhaC AGAUGCGUGagggA--gcGGGUUU--aAG--aguaA--GCGUUG--g--agGALGACAA--CGAGGA--UAAGCGC--CGaaaggAAAA--UUCgcca		
7*	BS IysC GGUGAGGAUagggUgcGAUCUUC--aAG--aguaU--GCCUUU--Gg--ag--AAAGAUGGA--UUCUGUGAA--AAAGGC--UGaaaggGGAGCG--Ucgcca		
8	CA IysA ACCUUUUGUGagggUgcUUUAAGUCaG--aGuaA--CGUUUG--g--ag--UUGGCA--AACUUAGA--UGAACGG--UaaaggGGCUUU--Agcca		
9	CP IysA GACCAAGUGagggUgcGUUAUU--aAG--agua--GUCUAU--Aglag--CUGACA--AG--9--UUAU--GaaaggGAU--AUGgcca		
10	CP IysP AACUGAGAUagggC--gcGALCAUU--aAU--agua--UCUUUG--Ag--ag--GUAAGCA--AUGAA--GCAAG--UGaaaggAUGA--AUGgcca		
11	CP nhaC AAAGAGGUGagggC--gcGAGUAUC--aAG--agua--CUAAAU--Gg--ag--UUAAGU--ACGUAGAGUUUAG--GaaaggGAUUAU--Cgcca		
12	EC IysC CAGGCCAGagggC--gcGUUGCCC--a----aguaACGGUGUG--g--ag--GAGCCAG--UCCUGUGA--UAACACC--UgGGUGCAUCgcca		
13	HI nhaC UACAAAGUGagggC--gcAAUUAU--aUA--agua--UUUUUG--Ag--ag--UGGAUA--CGAAGAA--GAAAAA--GaaaggAAUAGU--Ugcga		
14	OI dapa GUUUUGGAGagggUgcGGAGACC--aUC--agua--UUUUUC--GgAg--GGAUGAG--CGUAUG--GGAAG--GaaaggGGAA--UcUgcca		
15	OI nhaC UCGUGCGUGagggA--gcAUACAAC--aUU--agua--AUCCAG--Aag--agGALGACAA--CGALCAUA--GUUGU--GGaaaggGUUUU--Ugcga		
16	PM nhaC UACUUGUGagggUgcGALCACU--aUA--agua--UUUUUCU--g--ag--UGCAUA--CGAAG--GAAAAAG--GaaaggAGUAC--Cgcca		
17	SA IysC AUUUUUGAGagggC--gcAUCNAUC--aUG--agua--AGUUUA--g--aU--UACUGUCG--UAACAGC--UGAUUU--GaaaggGUEC--GAUgcca		
18	SA IysP AAUGAGUGagggUgcAUGUUUA--aUU--agua--ACUUGU--CagAg--UAUUUUG--UA--10--ACAAGU--GaaaggJAAAG--AUgcca		
19	SE IysC AGAUUUGAGagggC--gcAUCNAUC--aUG--agua--AACUUUA--g--aU--UAUUUCUGUAACAUAUJAGAUU--AaaaggUGA--GAUgcca		
20	SE IysP AAUGAGUGagggUgcAUUAUA--aUG--aCua--ACUUAU--CagAg--UUGUAUG--GA--10--AUAGU--GaaaggJAAUAU--gcca		
21	SF IysC CAGGCCAGagggC--gcGUUGCCC--a----aguaACGGUGUG--g--ag--GAGCCAG--UCCUGUGA--UAACACC--UGaaggGGUGCAUCgcca		
22	SO IysC AGGAACAGagggA--gcGUUAACU--a--Ggua--GUCAUUA--GAGg--agCAAAACUCCAGCA--UGAUUGAU--GAggga--UUAAGCgcca		
23	SO nhaC CCUUUAAGUGagggC--gcGUUGCCU--aUG--aCua--CUUGUGG--g--ag--GGUGAUG--CGGAGA--UGUACAAG--GaaaggAGU--CAGGgcca		
24	TM asd UGACCGAGagggC--gcGCCCGAG--aUG--agua--GGUGUCCC--7--g--ag--GAA--UCC--GGGACGGCU--GaaaggGAGGG--Cgcca		
25	TT IysA AGGUGAGGUGagggC--gcGGGUCAUGaG--aGua--ACAUGCC--Ag--ag--GUGUA--AG--10--GGUGU--GaaaggGGUG--CCGgcca		
26	TT psfP CGCAUAAUAGagggA--gcUGCCAAGCaU--gduUUUGCCAG--10--gAgAACCUCCAUA--CUCCUG--AAGaaaggUUUGG--Ugcga		
27	VC IysC UCUAGCAGagggA--gcACUGCCC--aGGCag--aUGUUUGG--g--agCCUCAACUCCA--UACAGAACAUCagggGGAGUAGUgcca		
28	VC nhaC UUUCCCGUGagggA--gcGGUUAOC--aAA--agua--UCCAGAUU--g--Gg--GLGAGC--CAUUG--AAUUGUGA--AaaaggGUU--GCCgcca		
29	VC nhaC CCUUUAAGUGagggC--gcGUGUUG--aUG--aguaC--CCAGUC--gUag--GUAGACCC--GAUG--AUCACUGG--UUaaaggGU--ACAGGgcca		
30	VV IysC UUUUGCAGagggA--gcACUGCCC--aGGCag--aUGUUUGG--g--agCCGCAACUCCA--CACAGAACAUCagggGGAGUAGUgcca		
31	VV nhaC UAUCCAGUGagggC--gcAUGGUA--aAG--agua--ACUAUAUU--g--Gg--GUGAU--GCCAAUGAAUAUAGU--GaaaggJAU--CCAUUgcca		

FIG. 18A

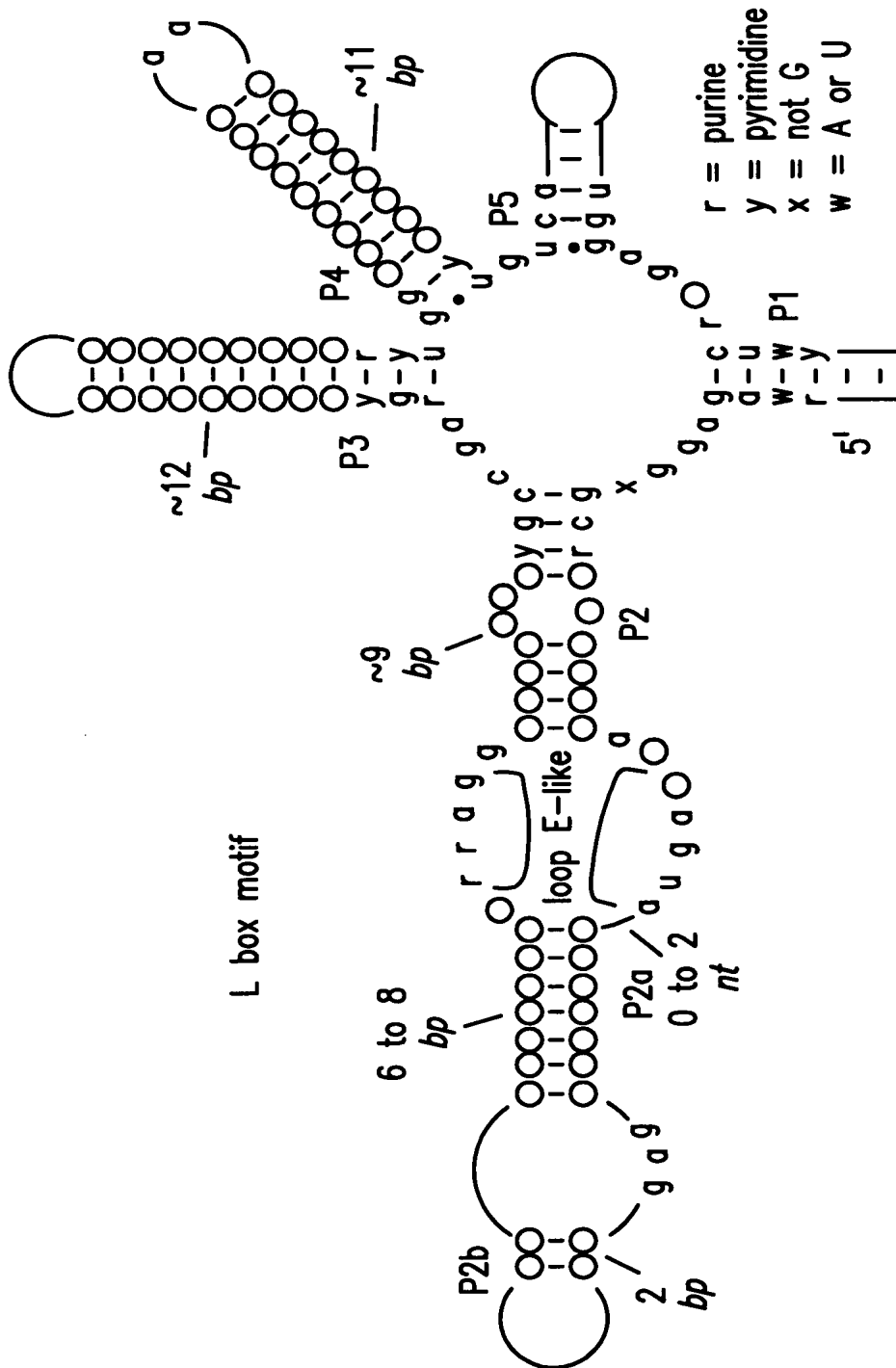


FIG. 19A

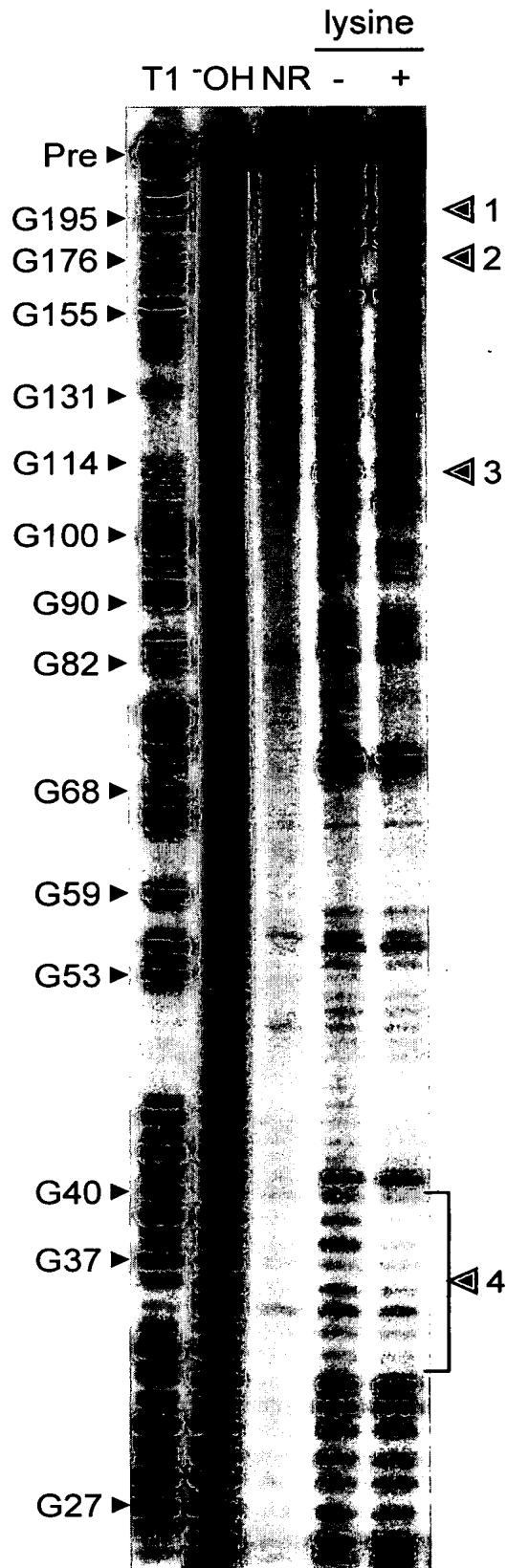


FIG.19B



FIG. 19C

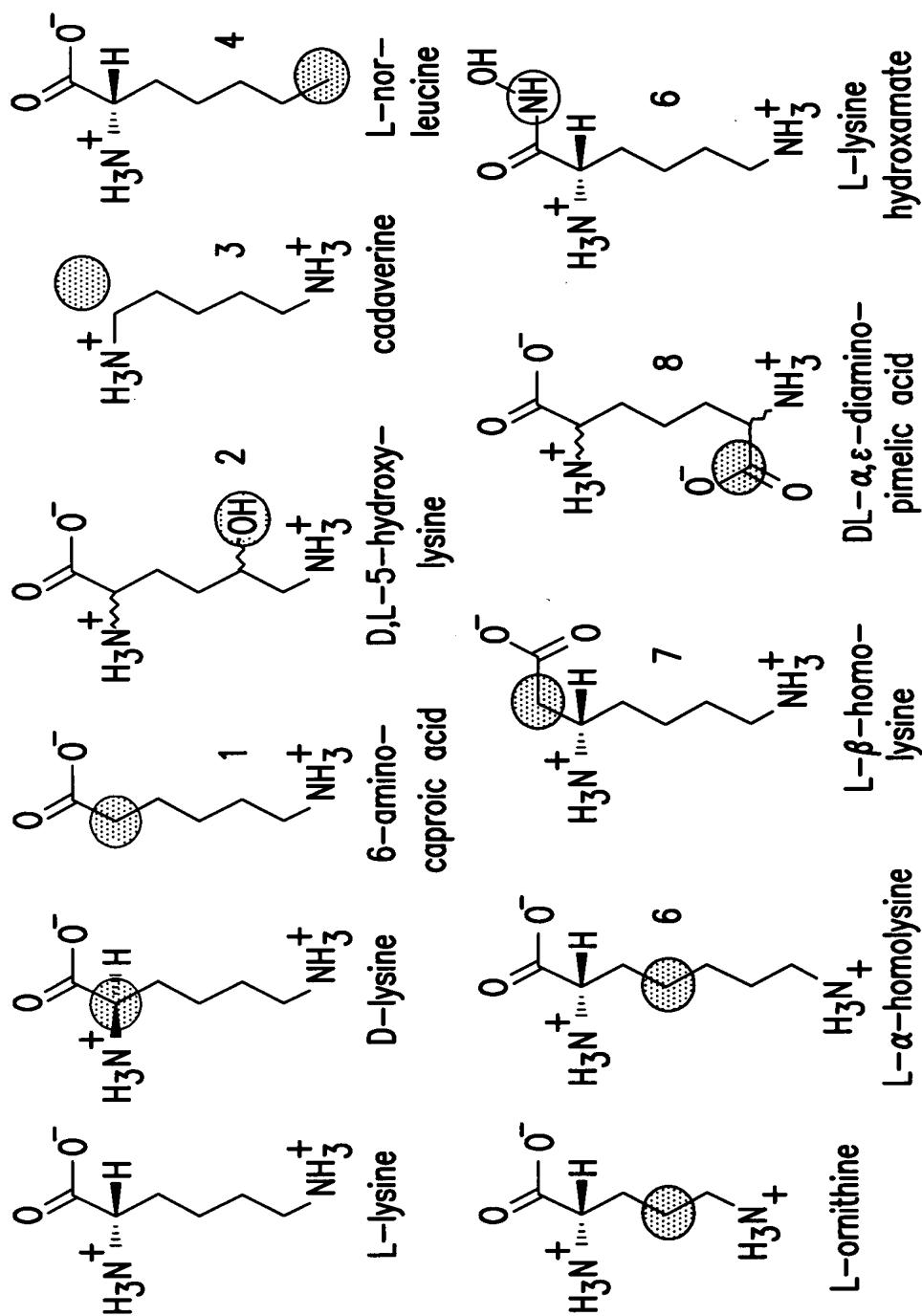


FIG. 20A

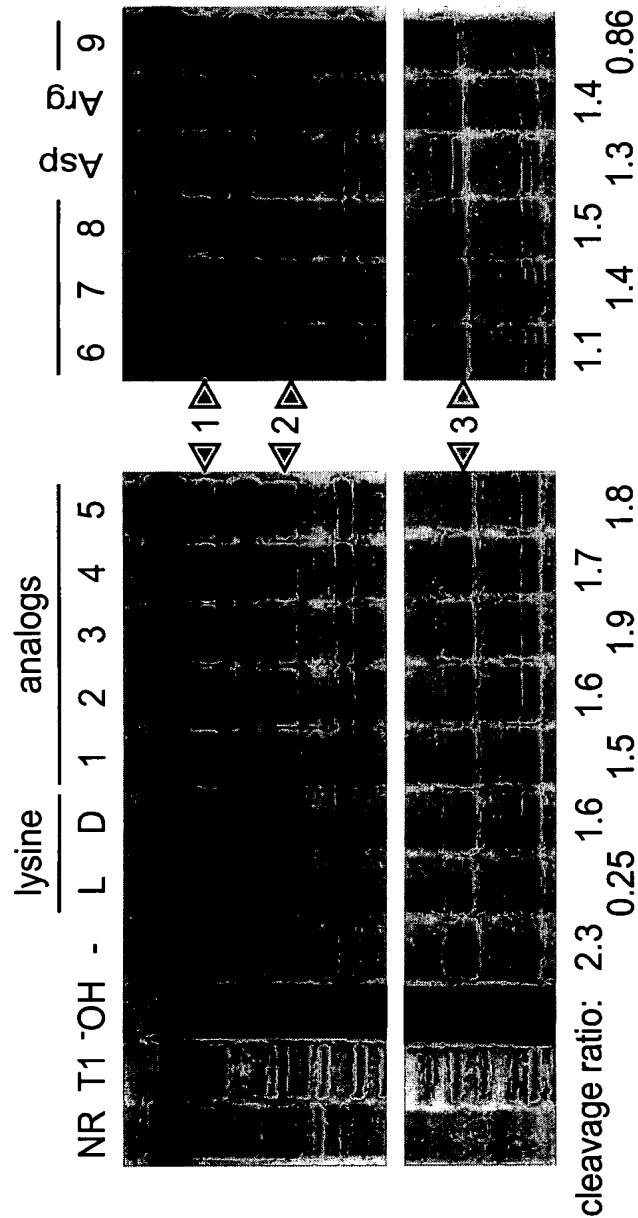


FIG.20B

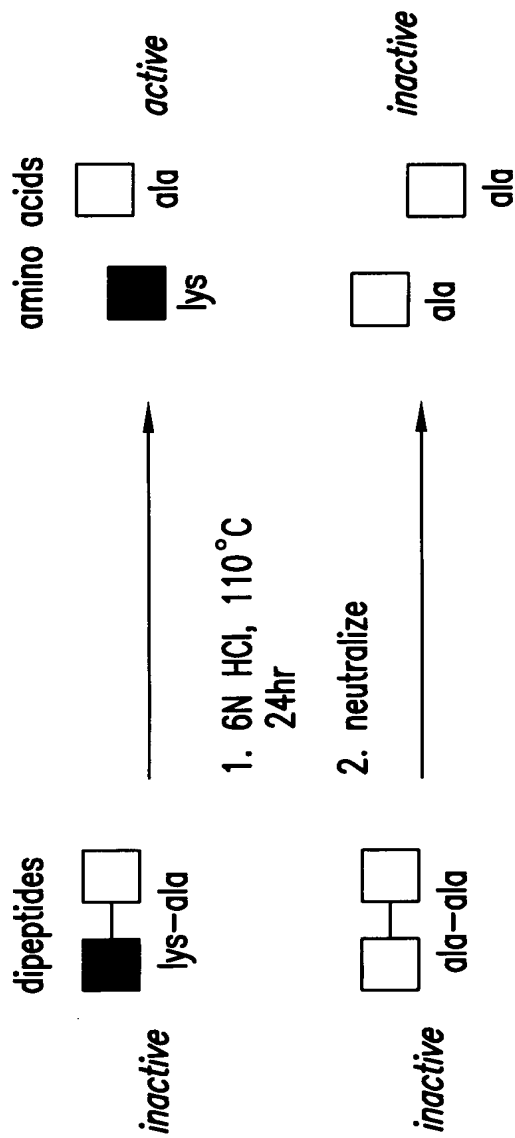


FIG.20C

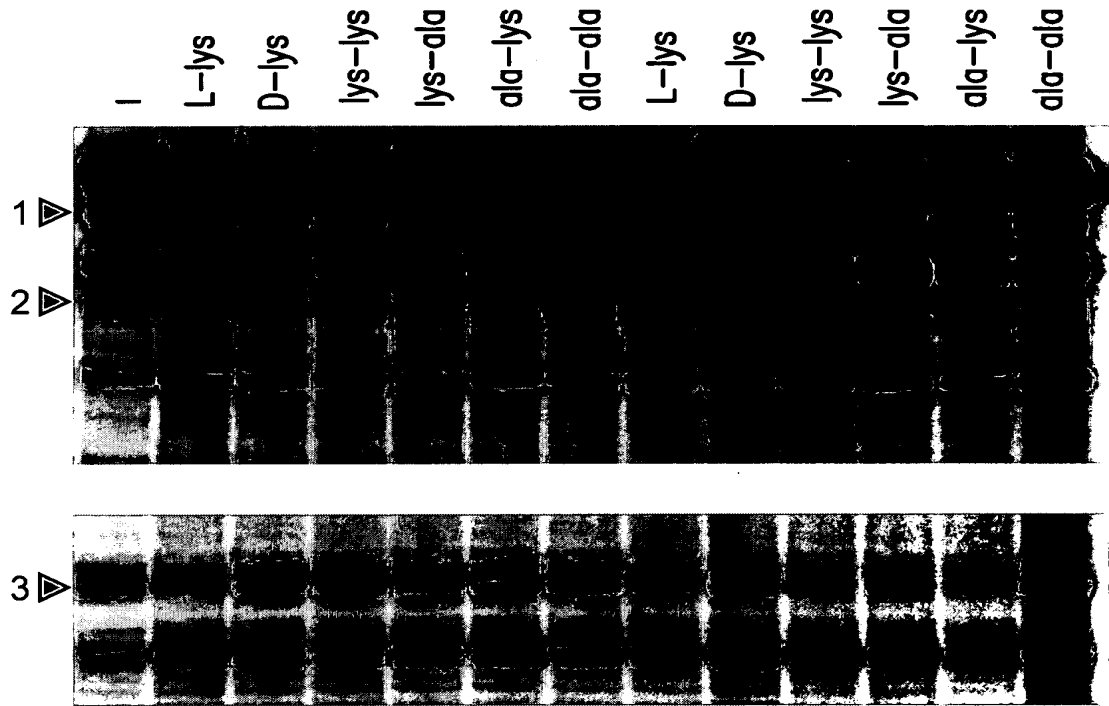


FIG.20D

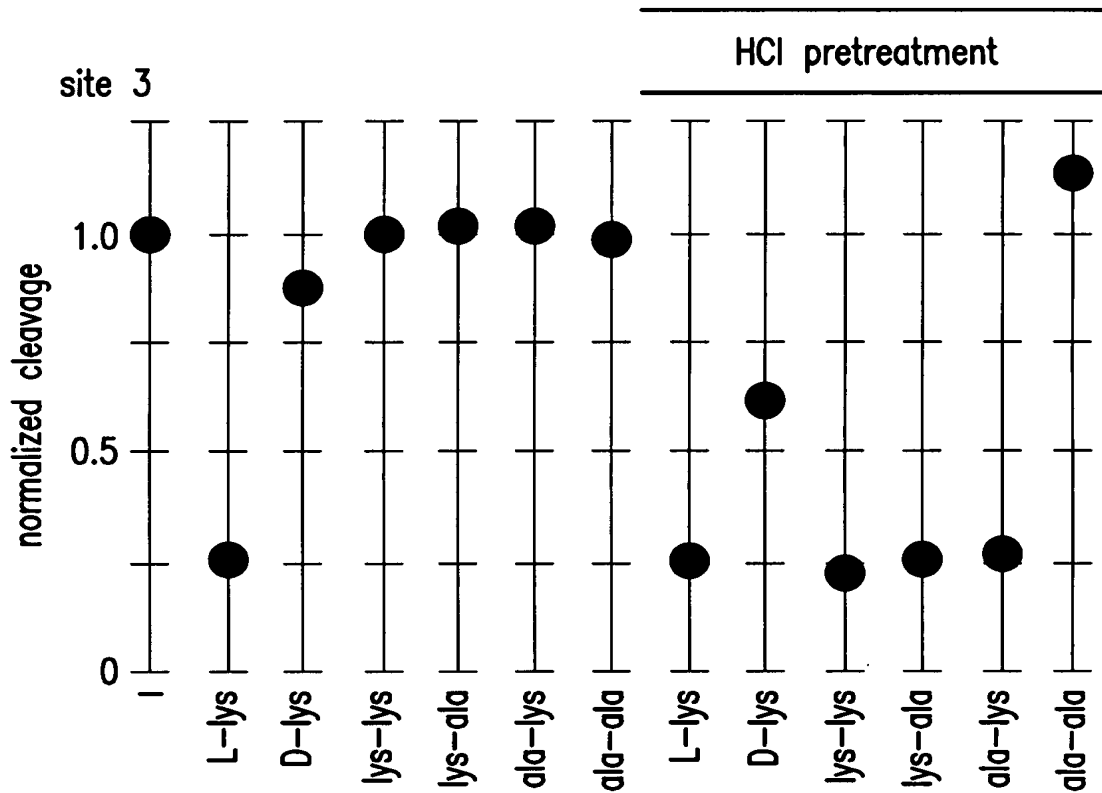


FIG.20E

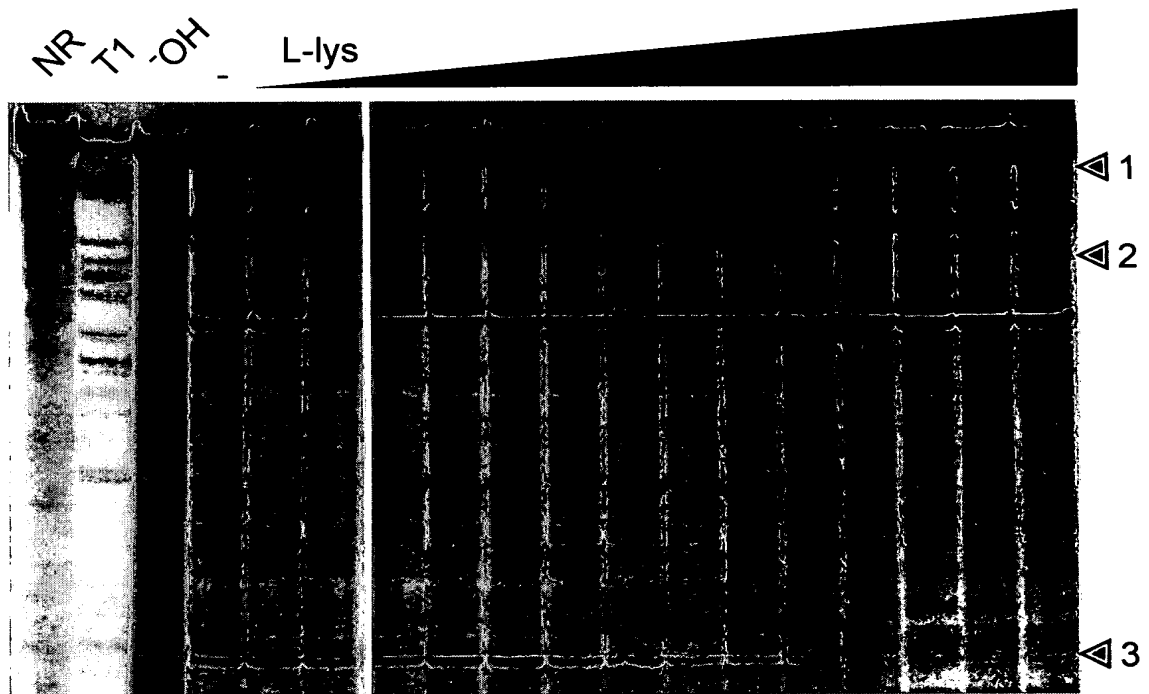


FIG.21A

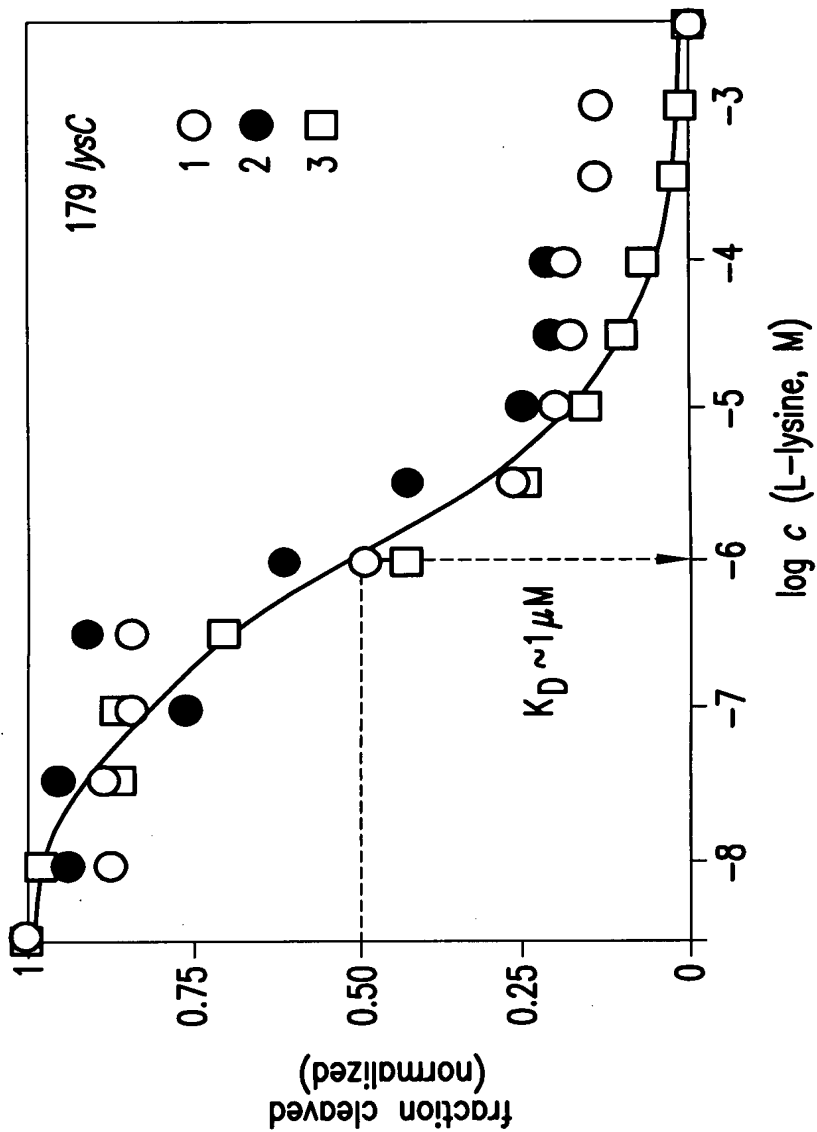


FIG. 21B

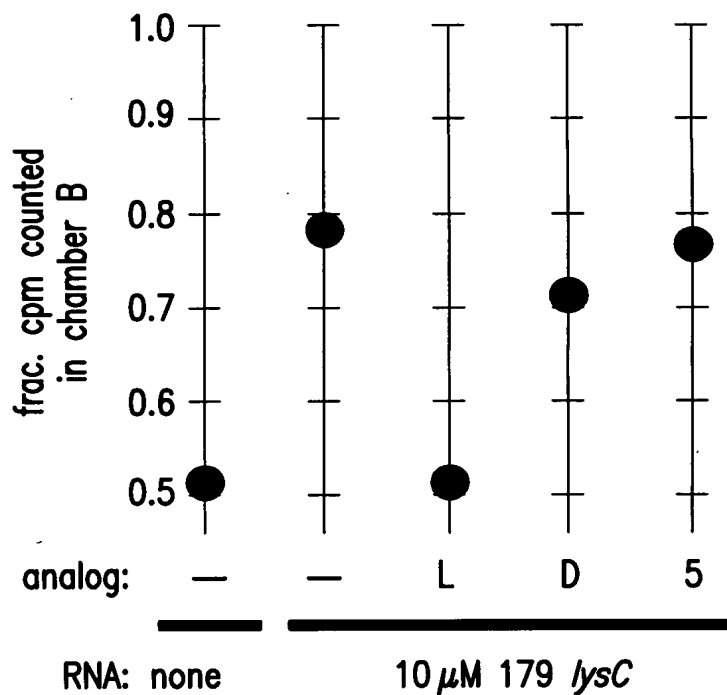


FIG.21C

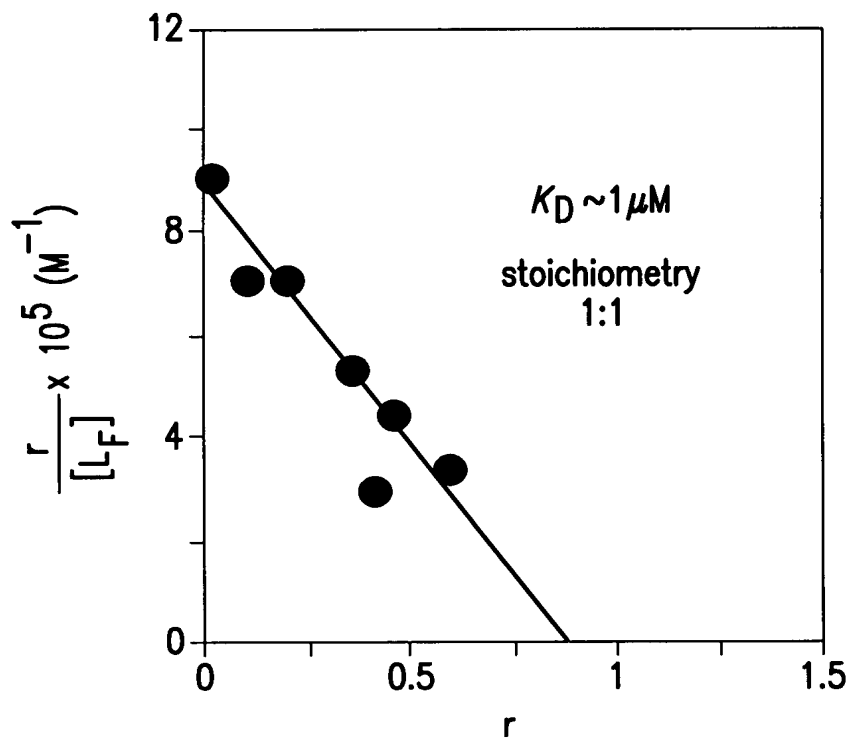


FIG.21D

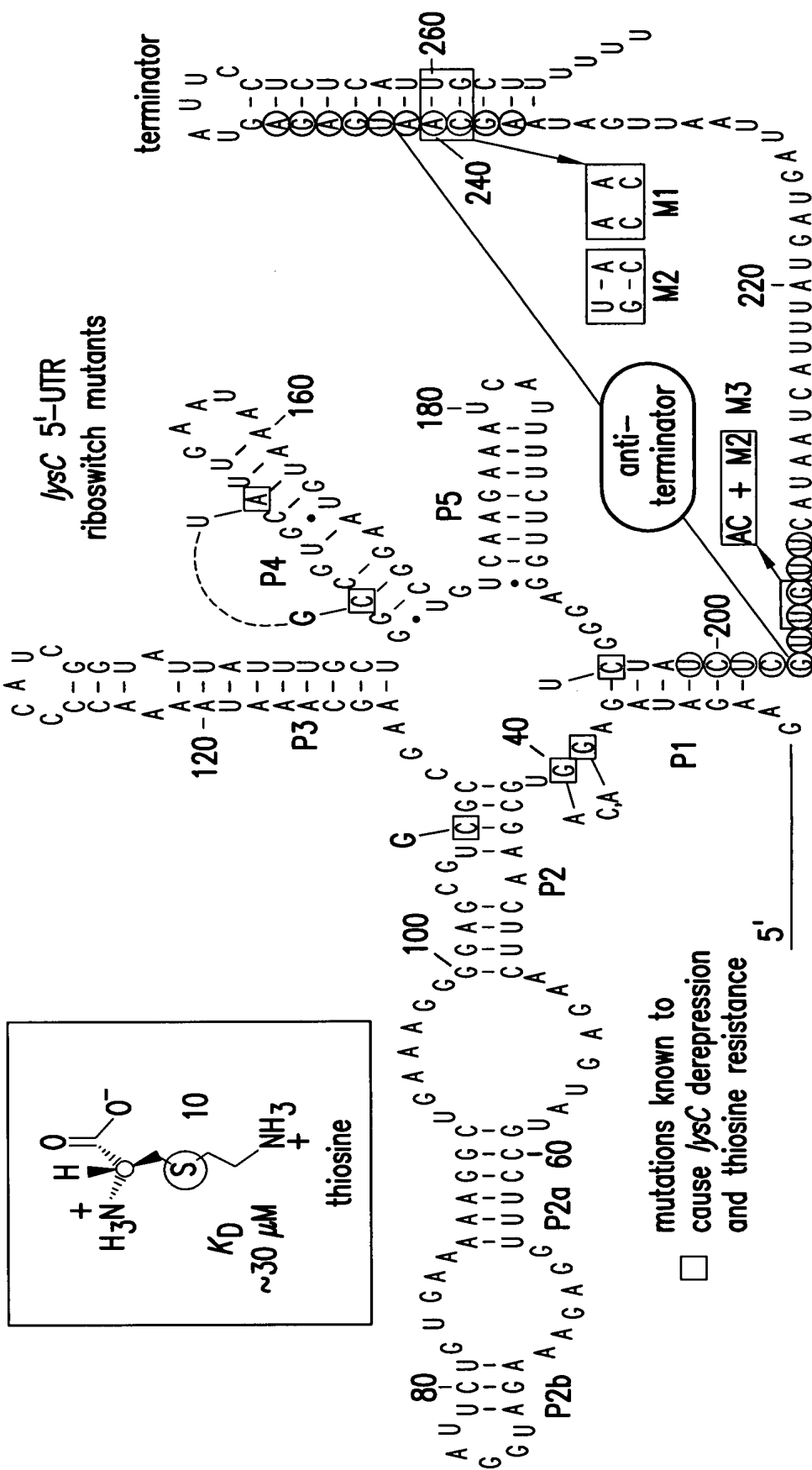


FIG. 22A

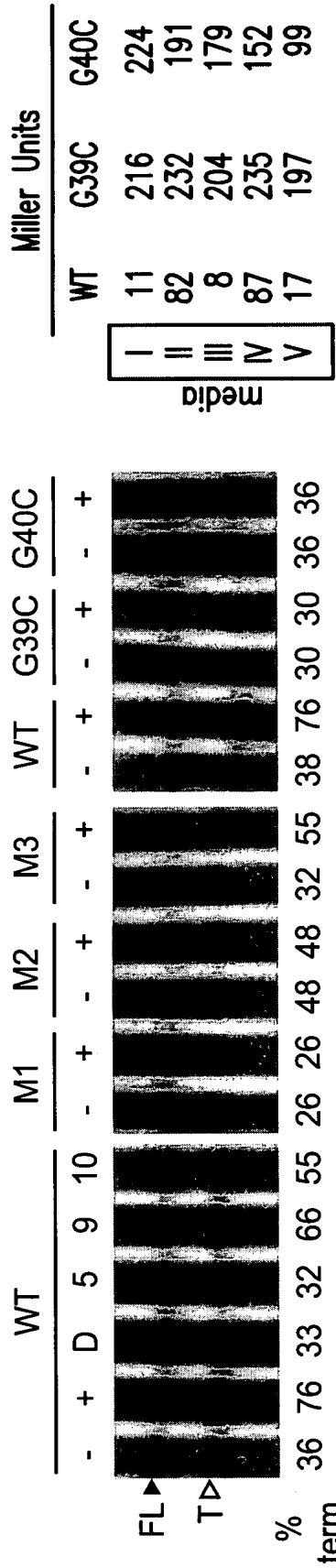


FIG.22B

FIG.22C

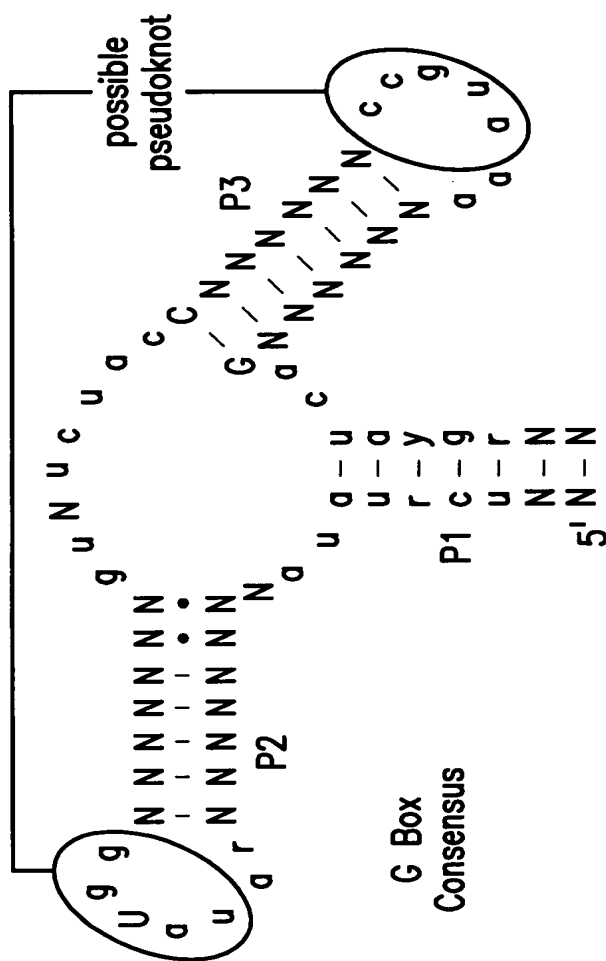


FIG. 24A



FIG. 24B

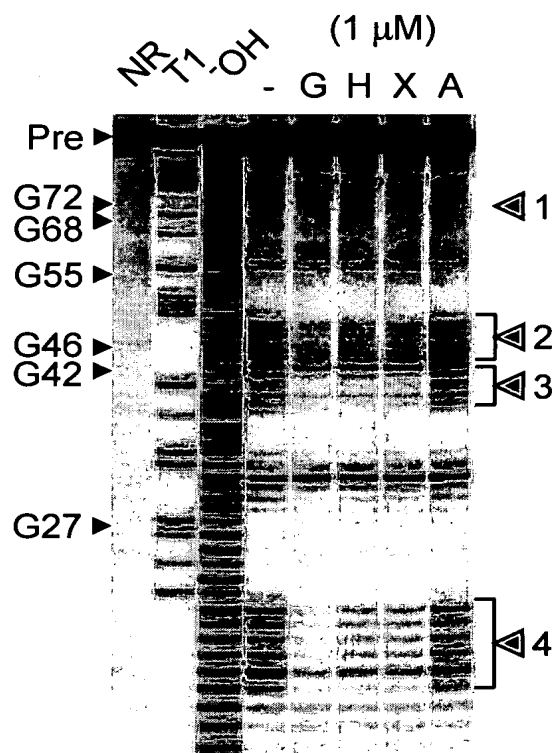


FIG.24C

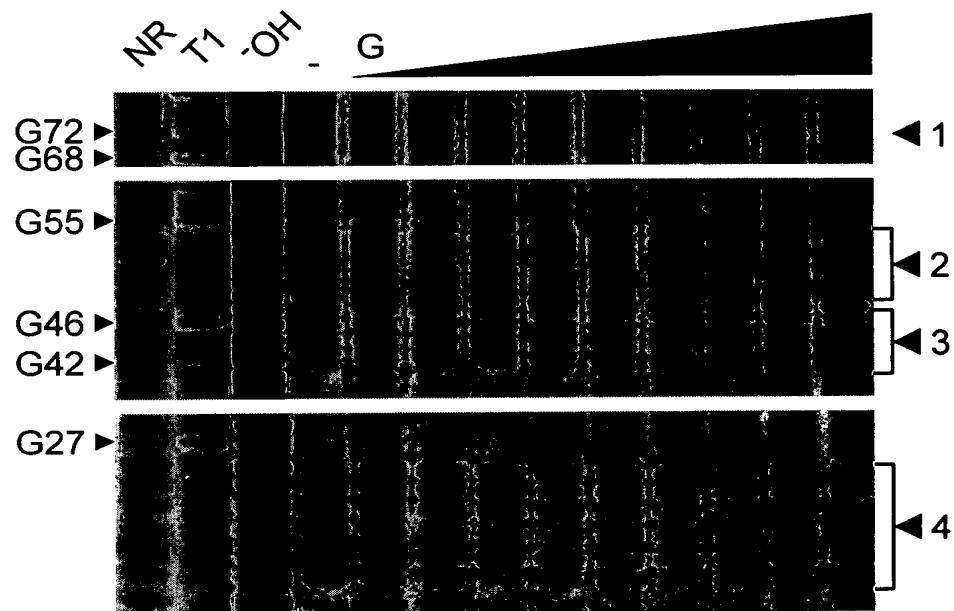


FIG.25A

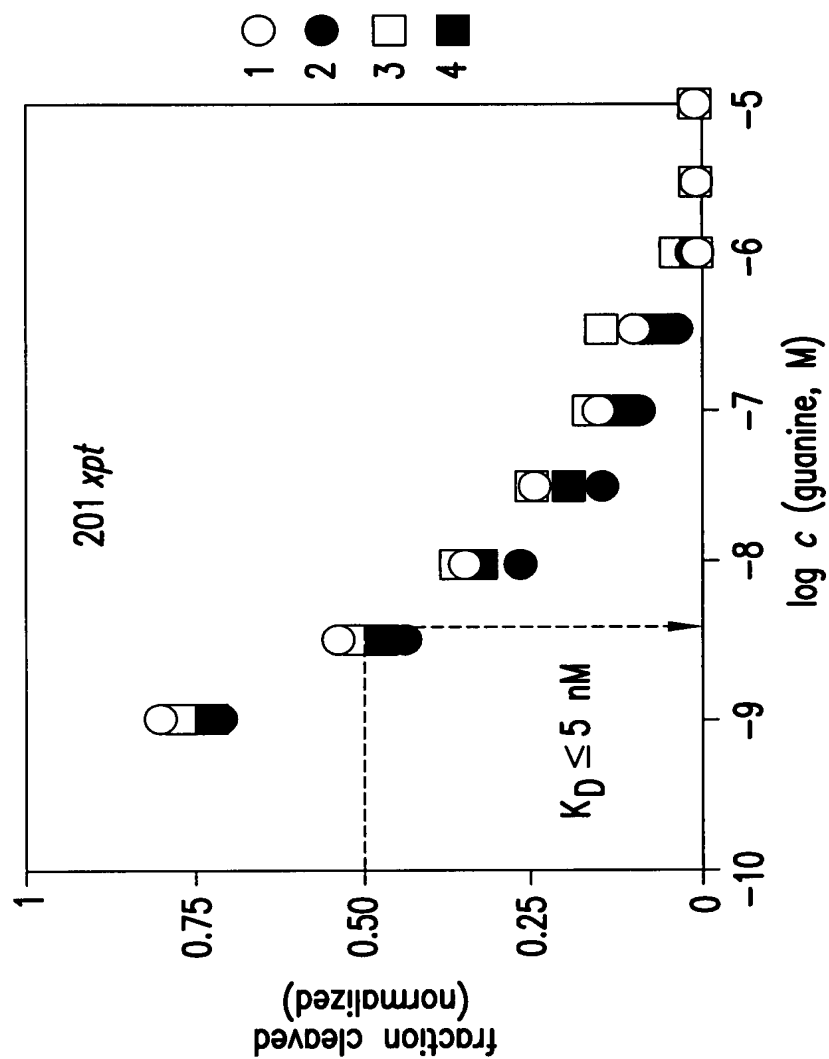


FIG. 25B

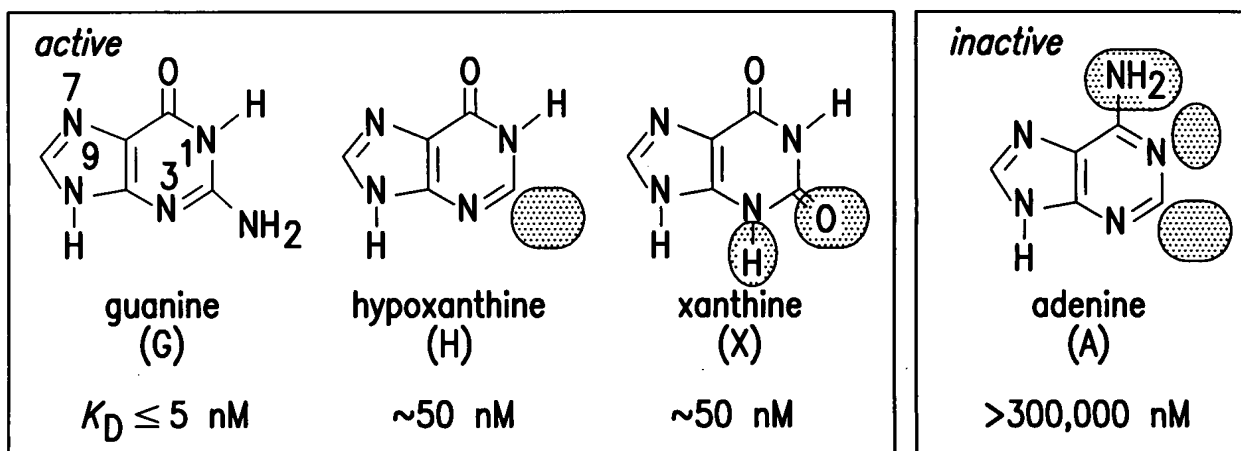


FIG.26A

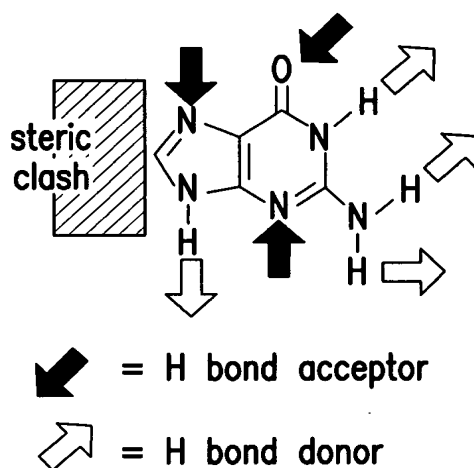


FIG.26C

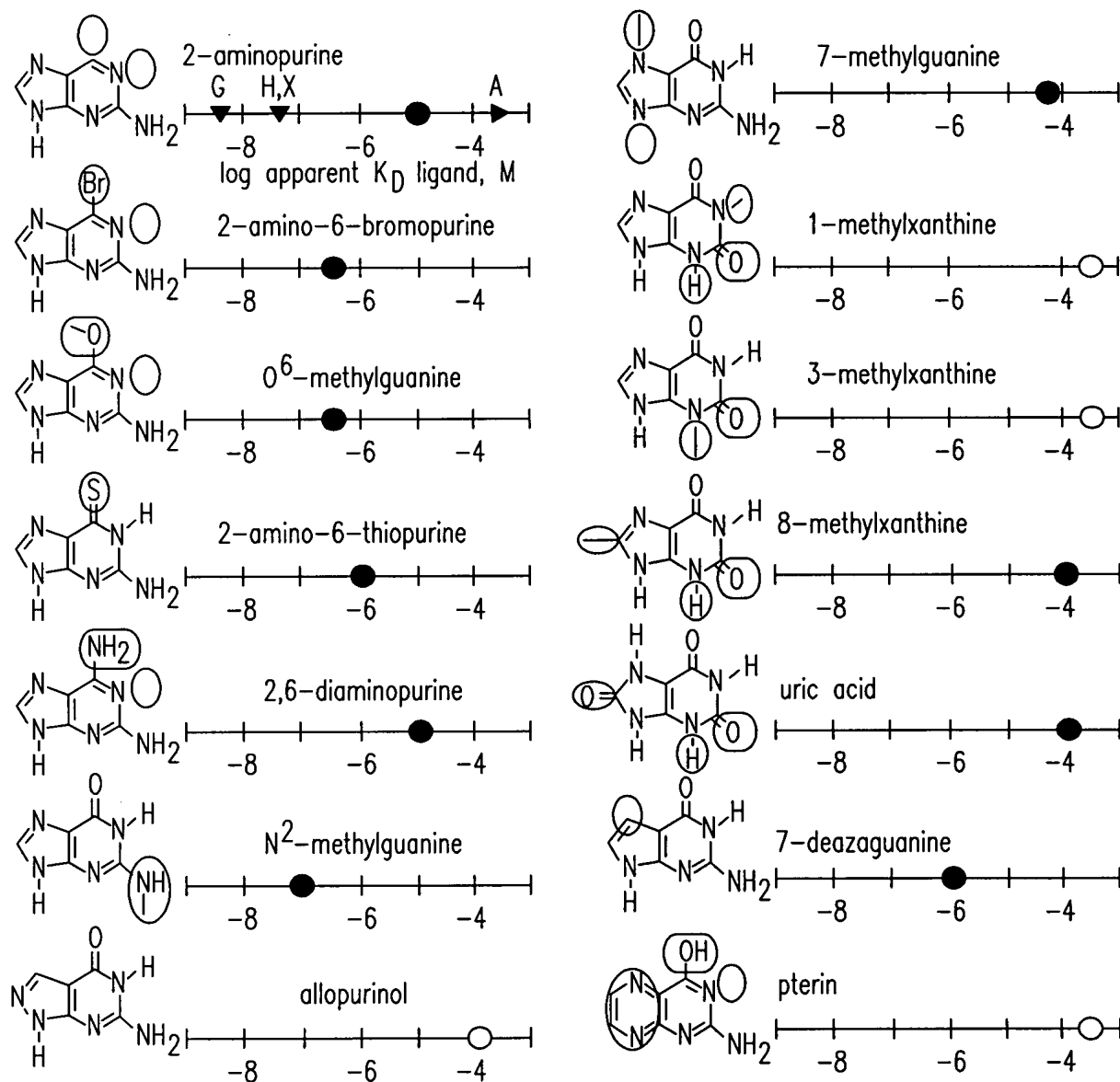


FIG. 26B

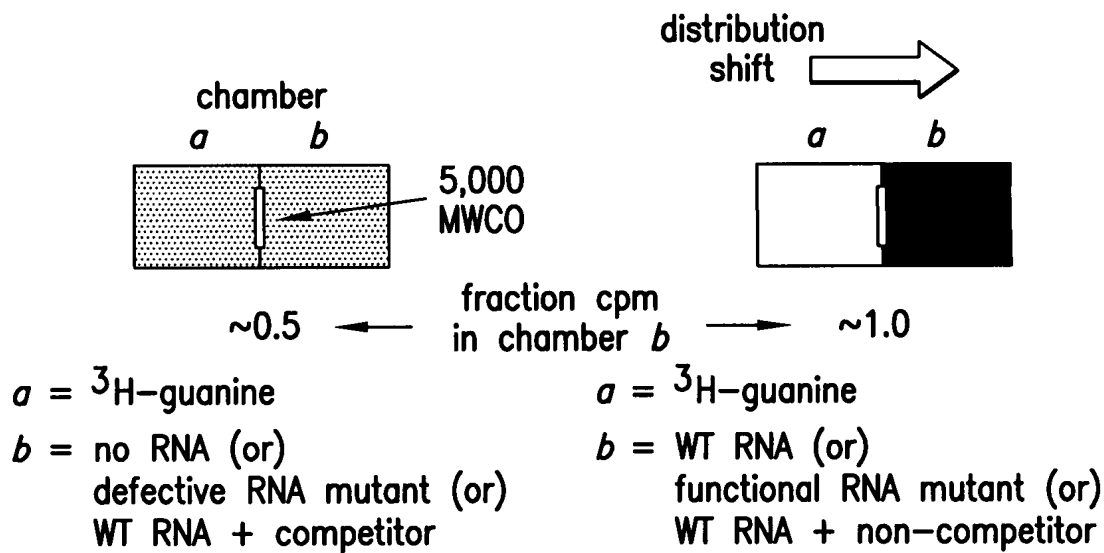


FIG.27A

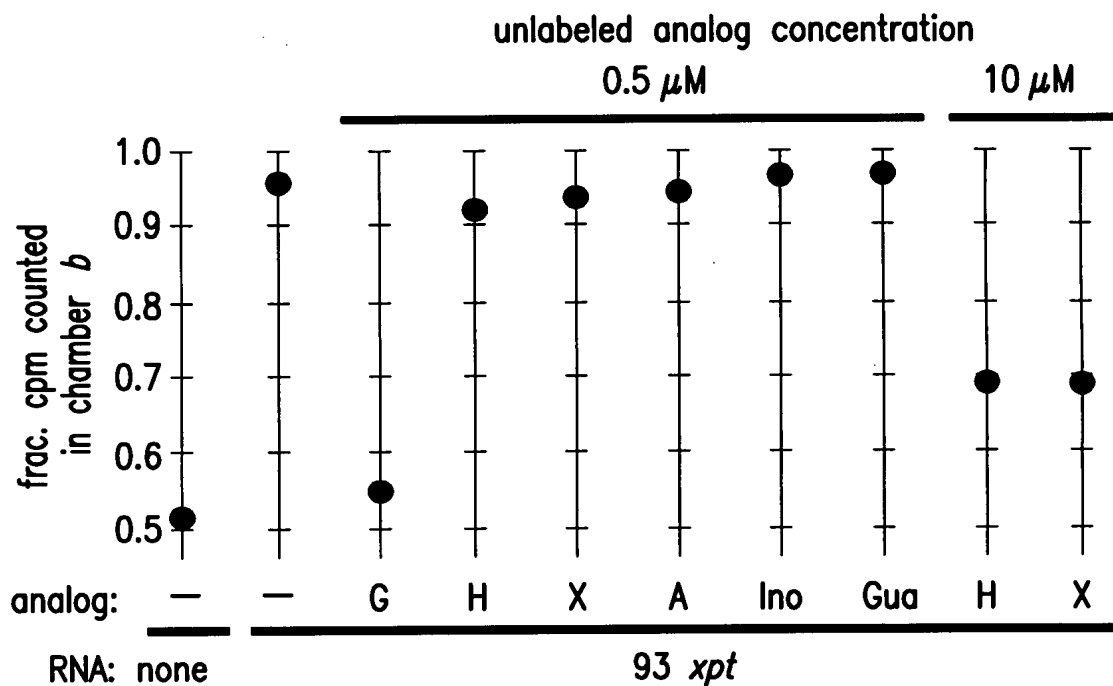


FIG.27B



FIG. 28A



FIG. 28B

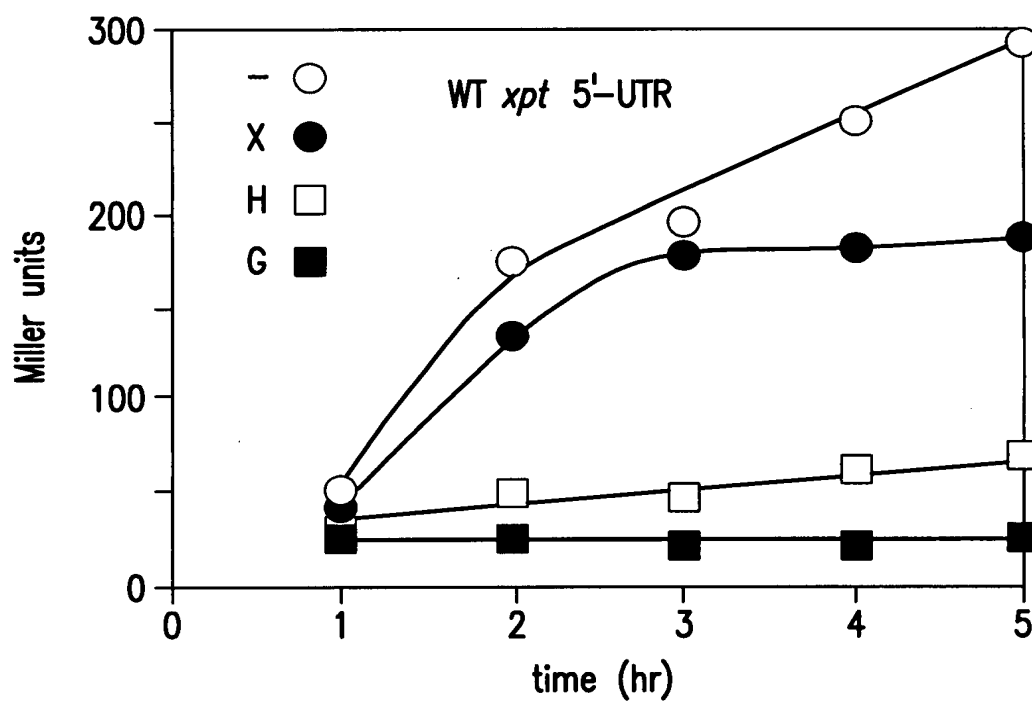


FIG.28C

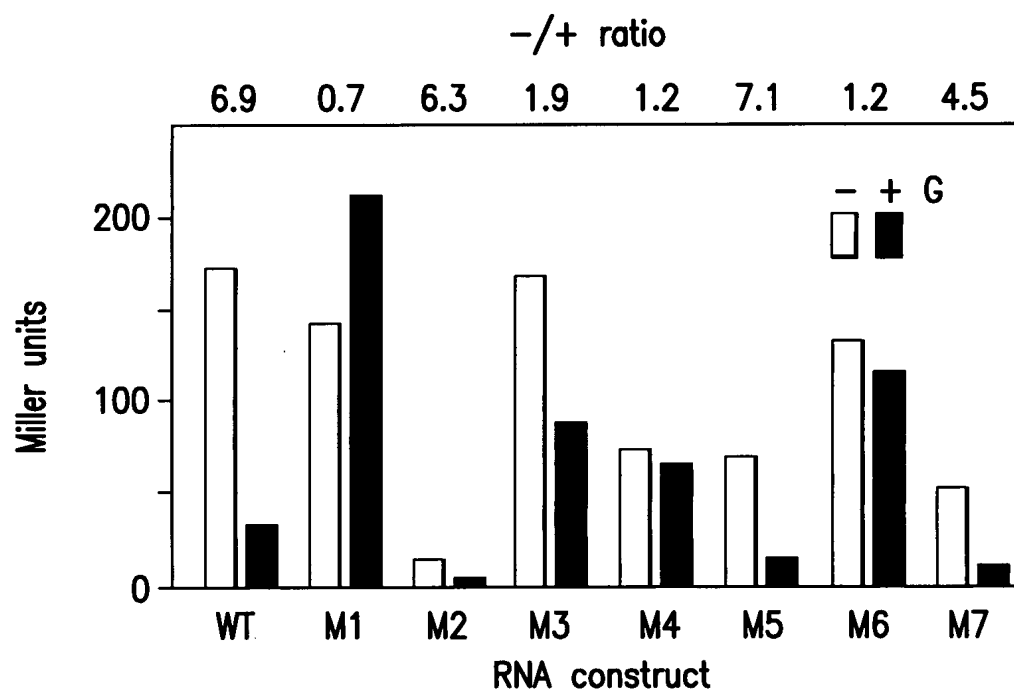


FIG.28D

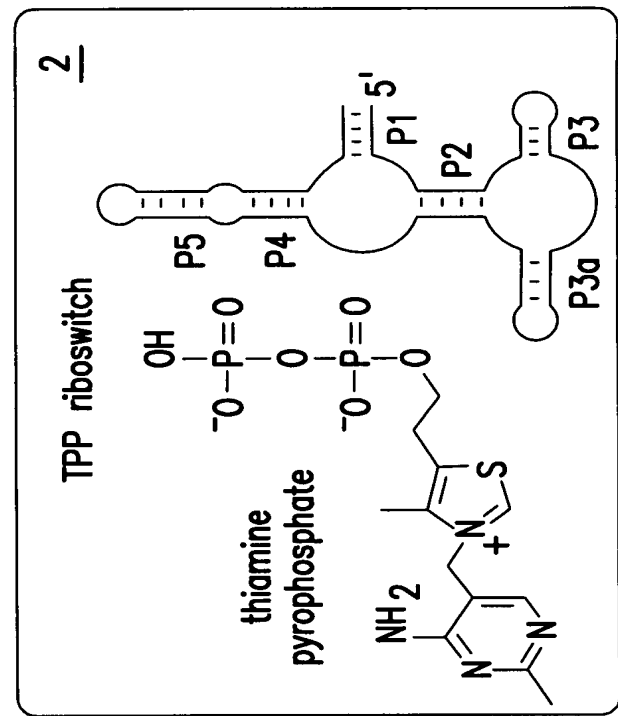
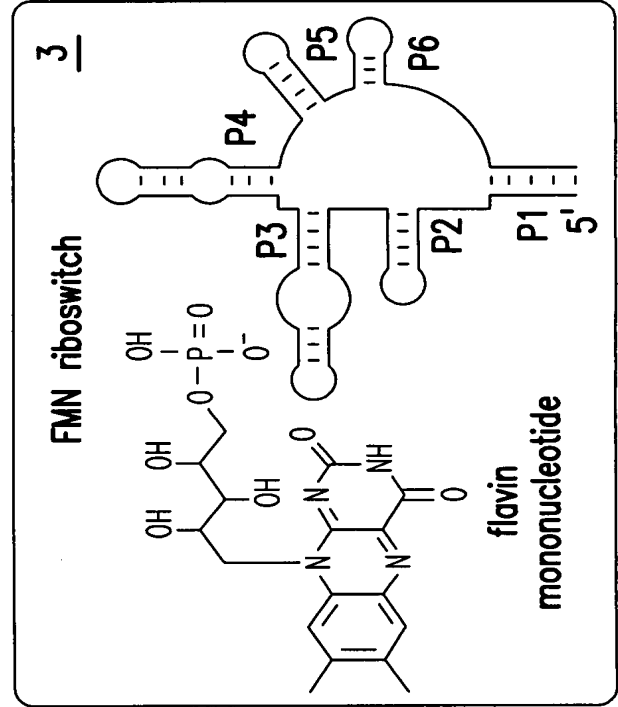
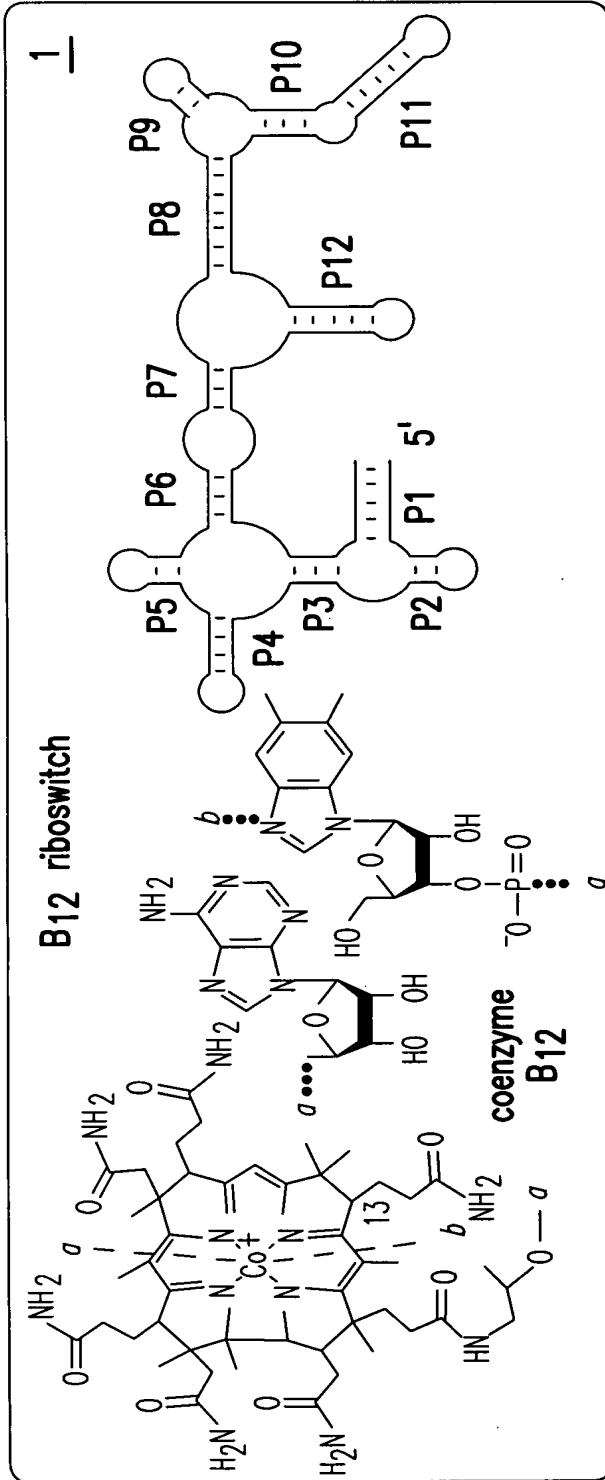


FIG. 29A

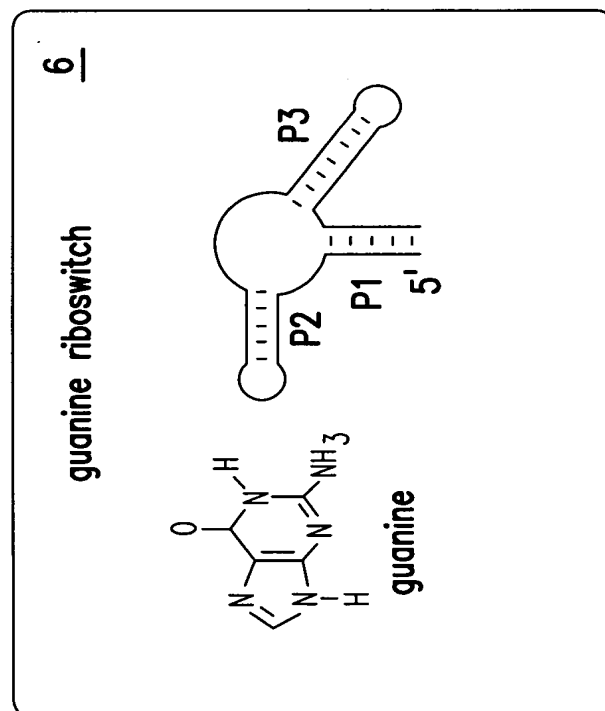
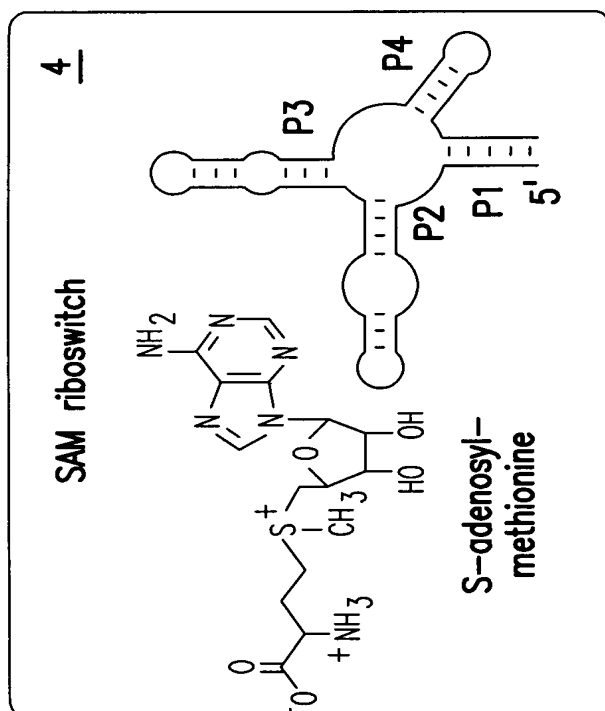
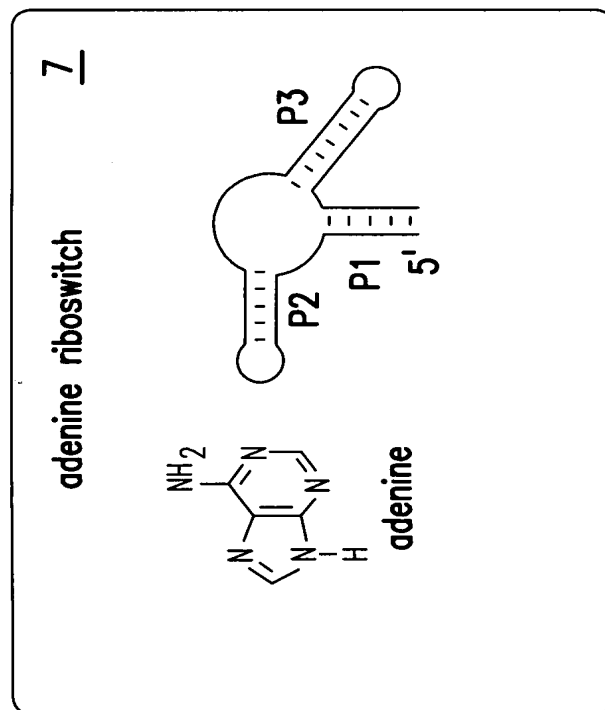
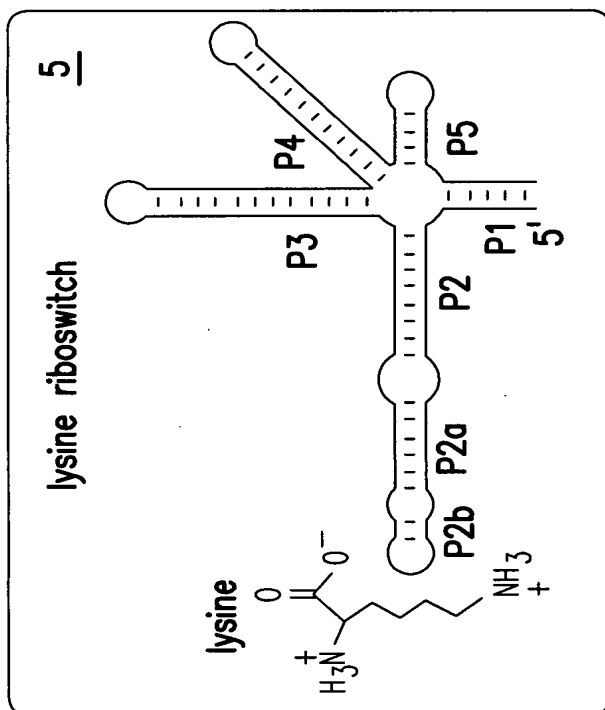


FIG. 29A-1

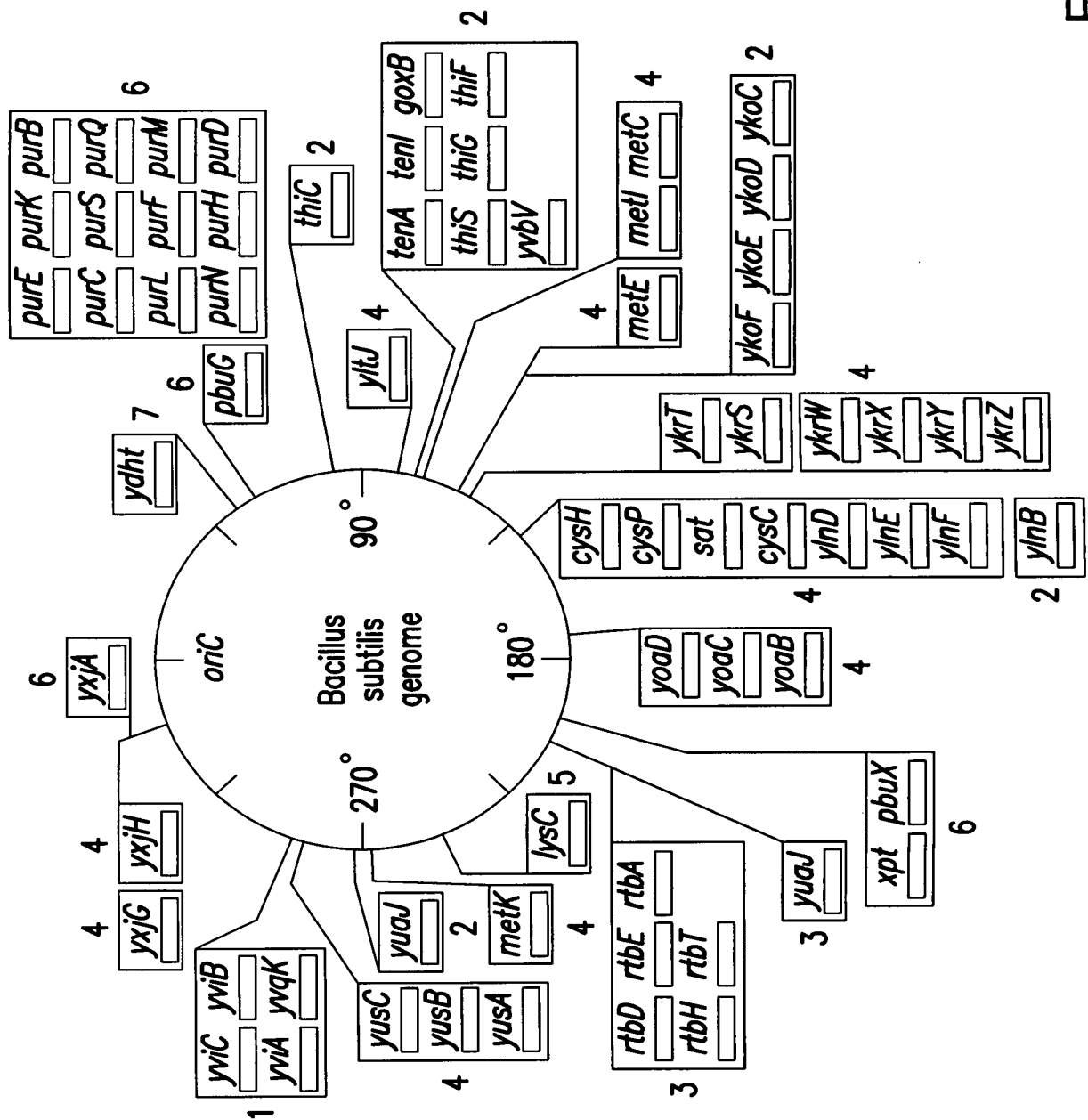


FIG.29B

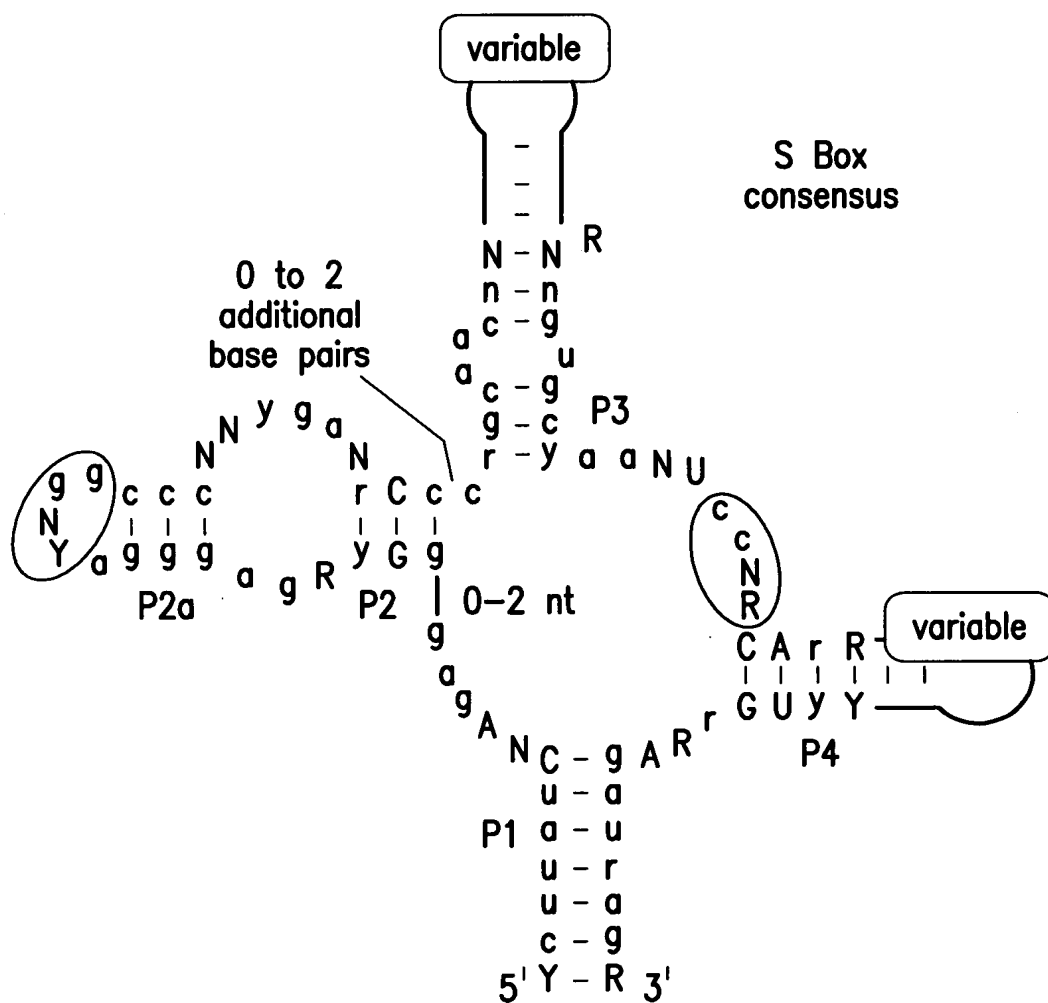


FIG.30A

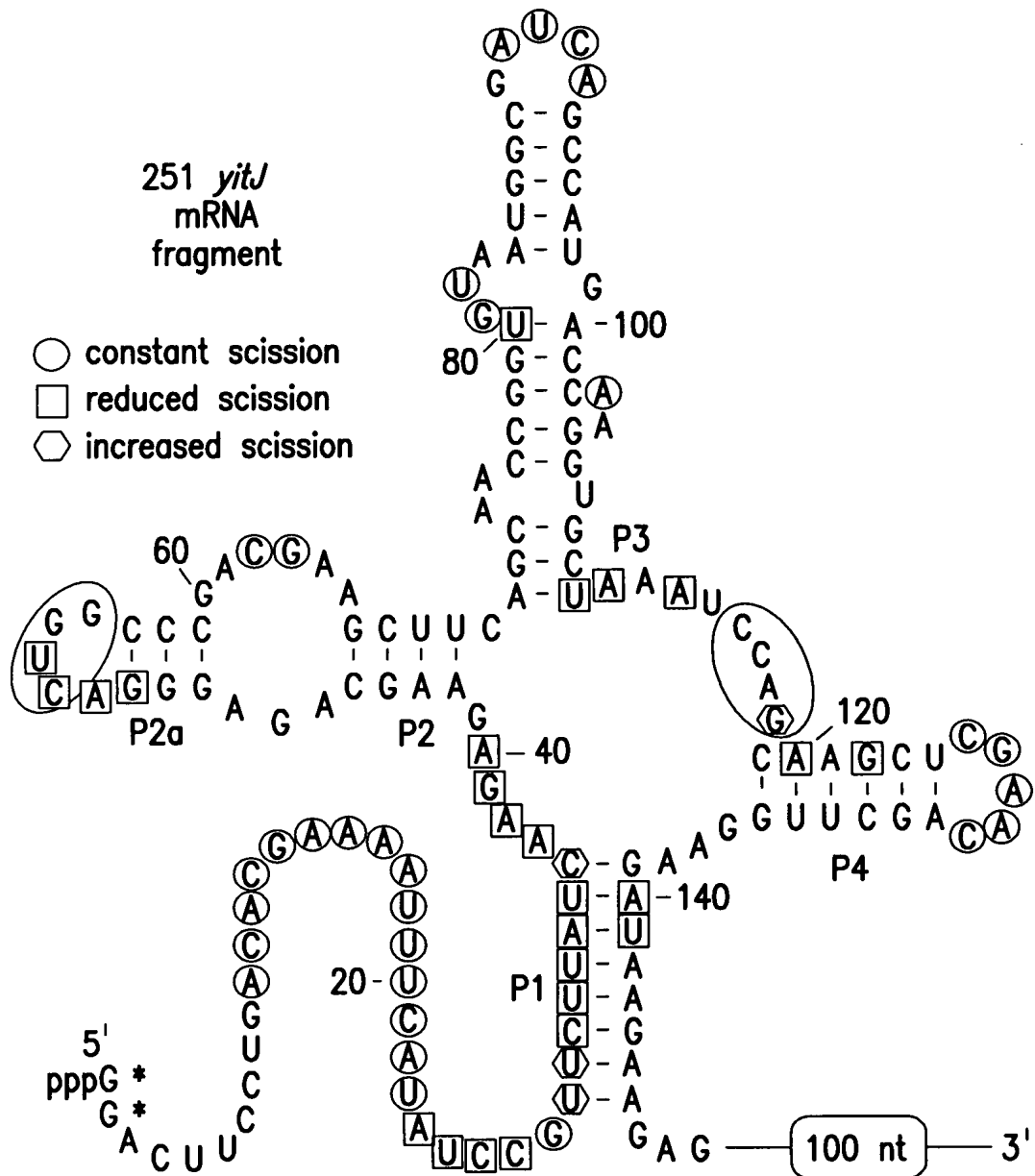


FIG.30B

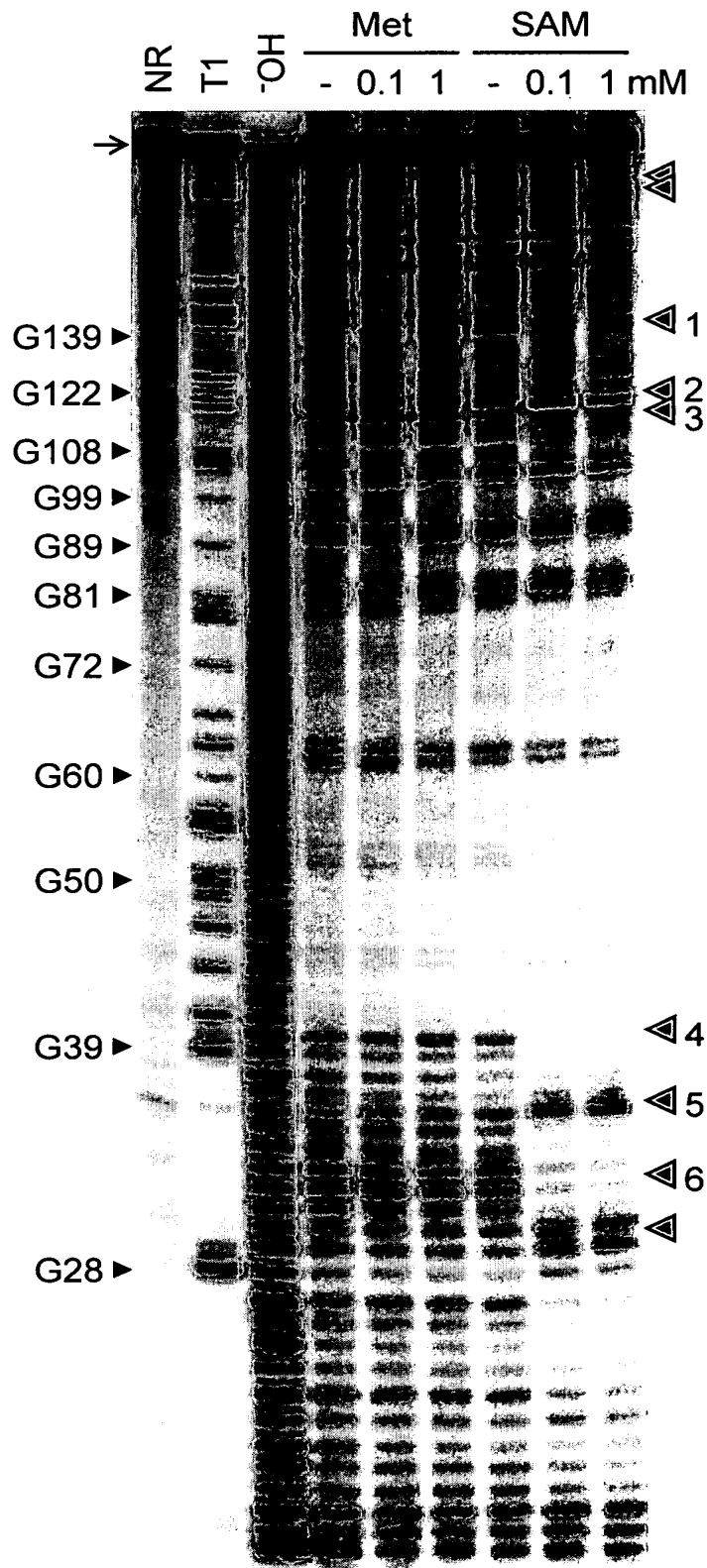


FIG.30C

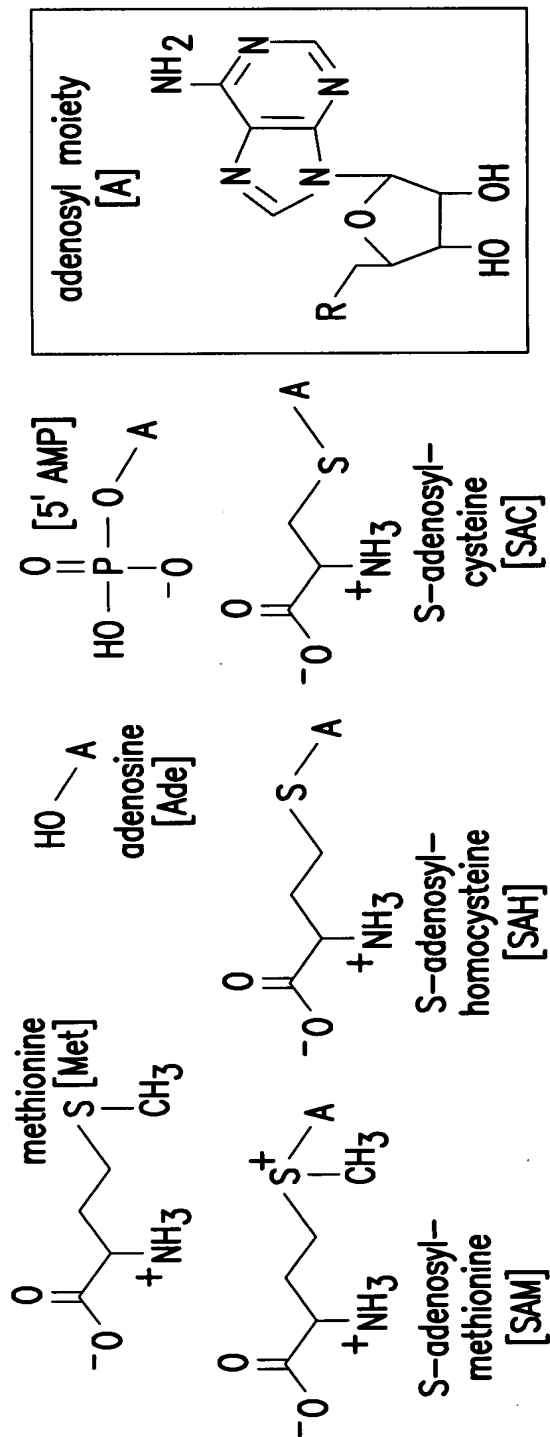


FIG. 31A

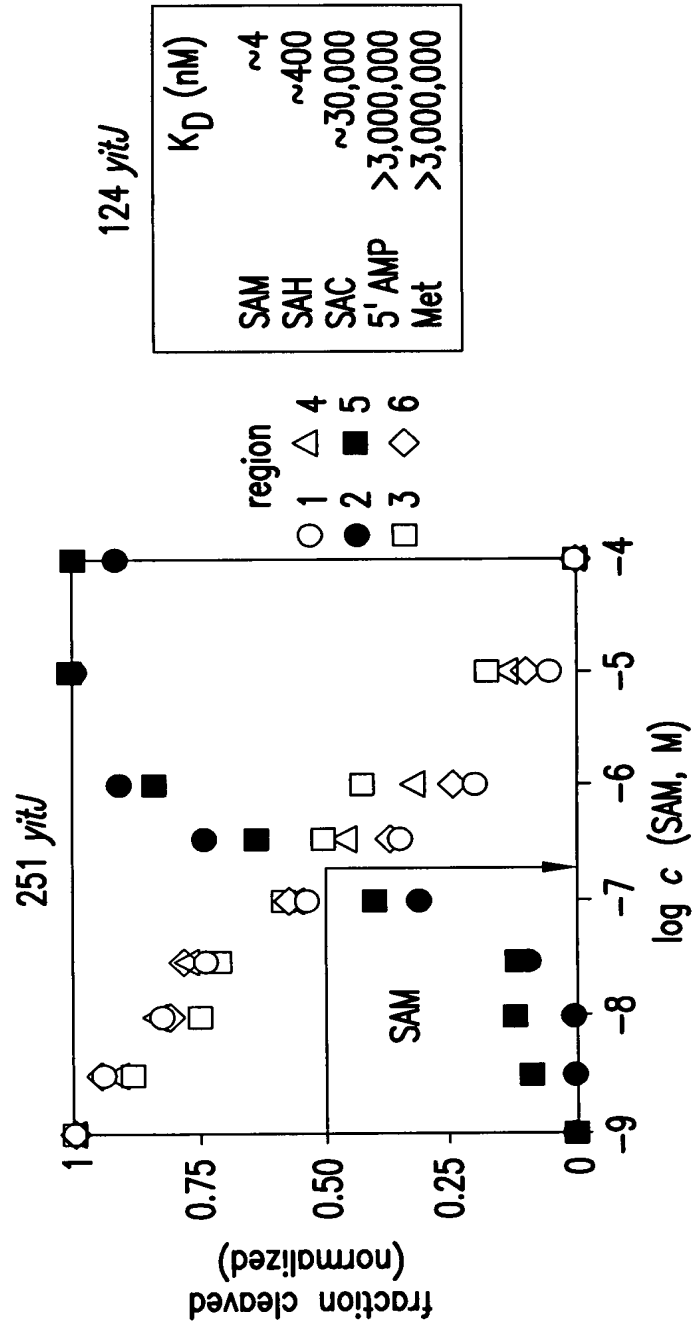


FIG. 31B

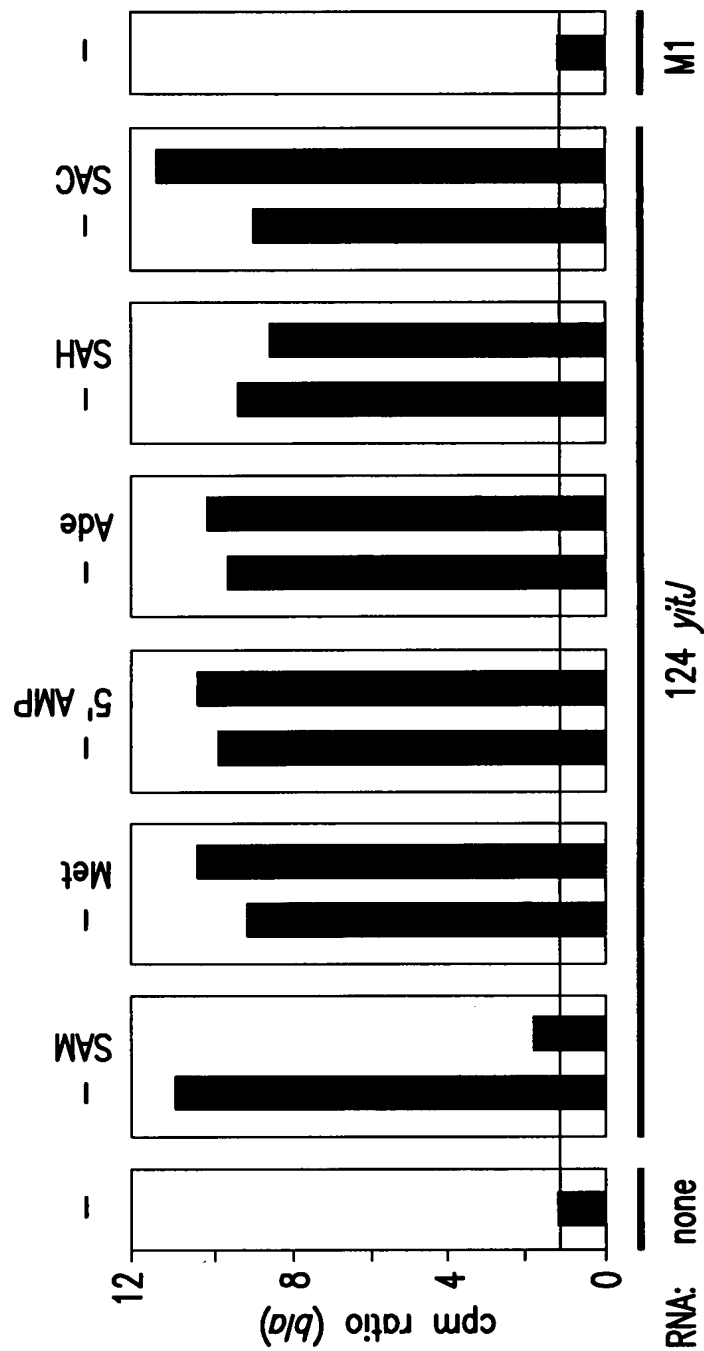


FIG.31C

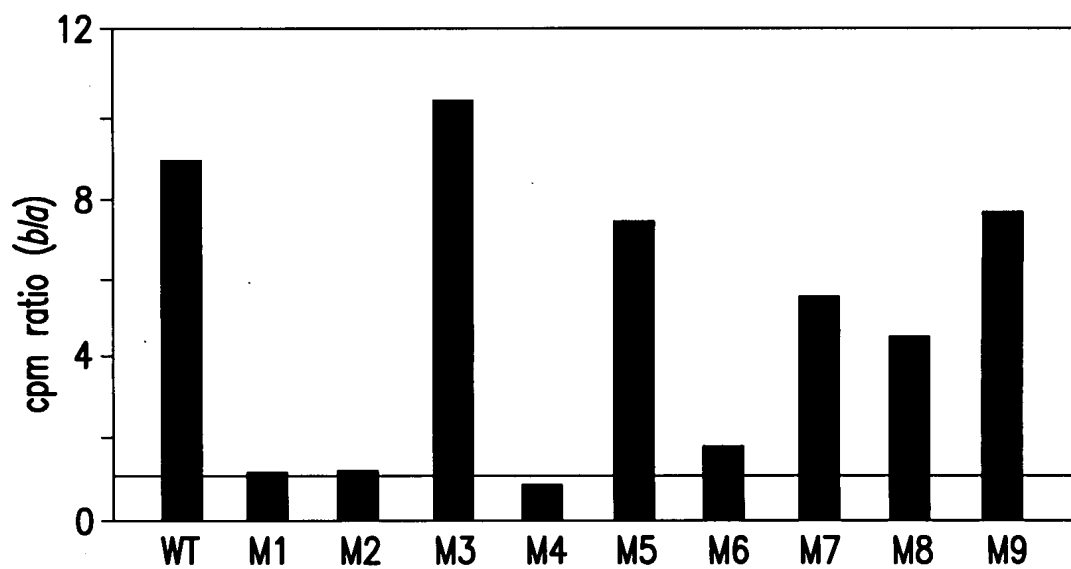


FIG.32B

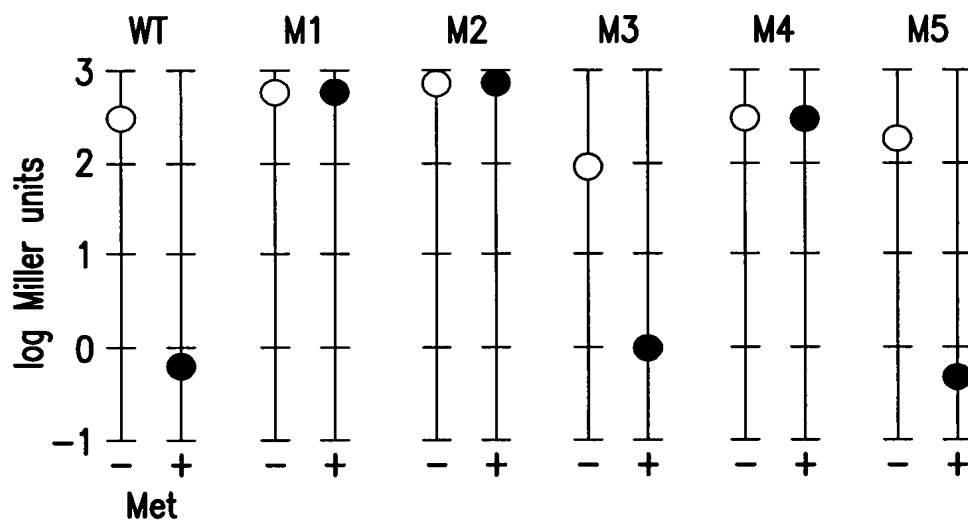


FIG.32C

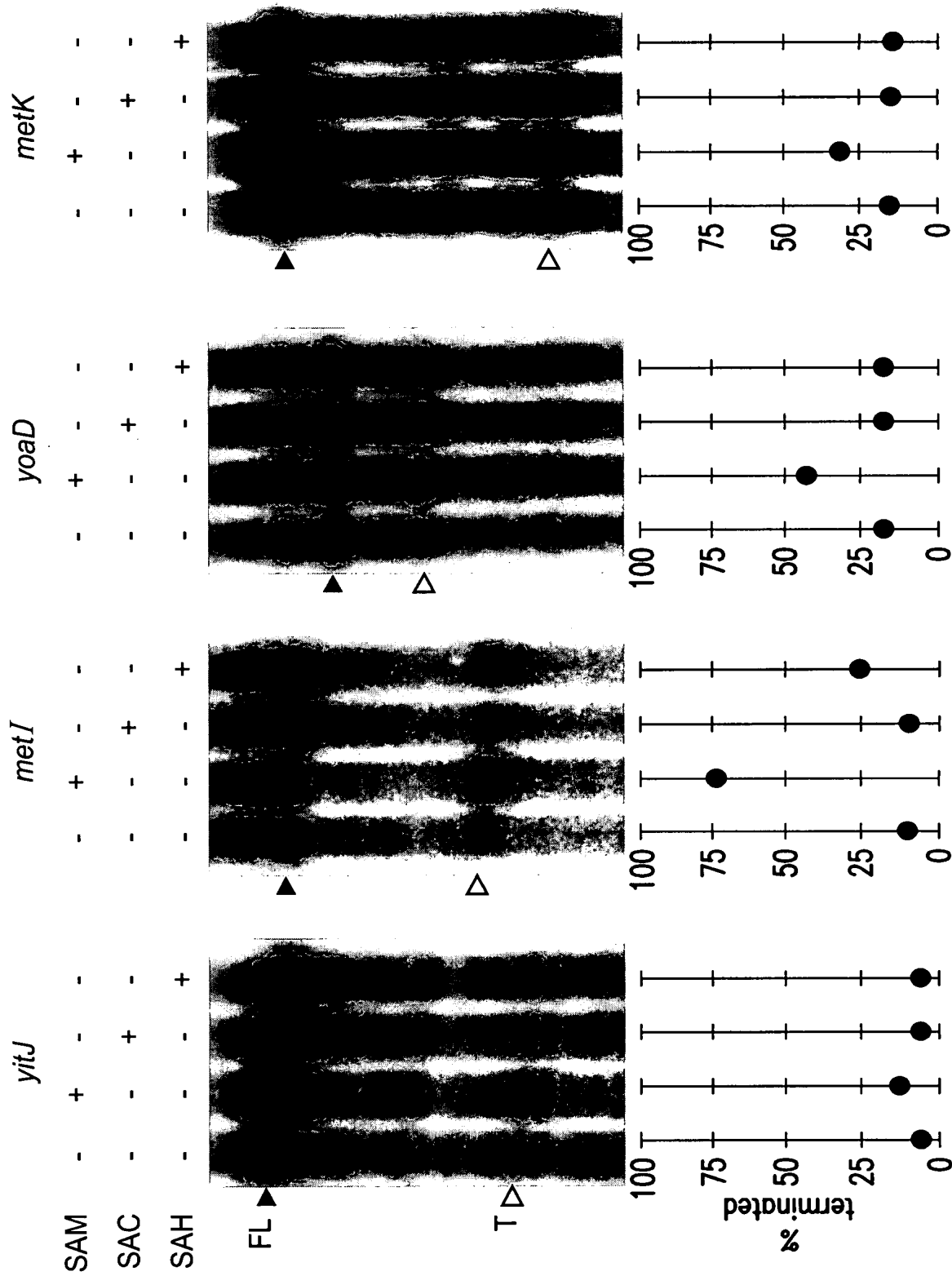


FIG.33A

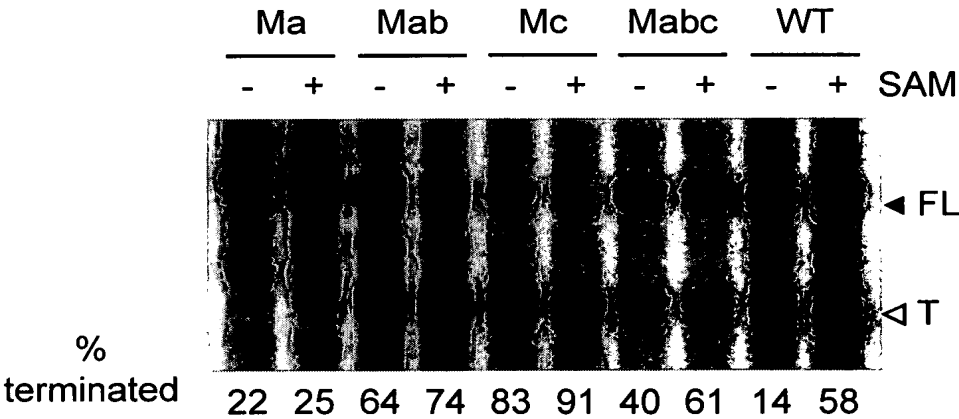


FIG.33B-1

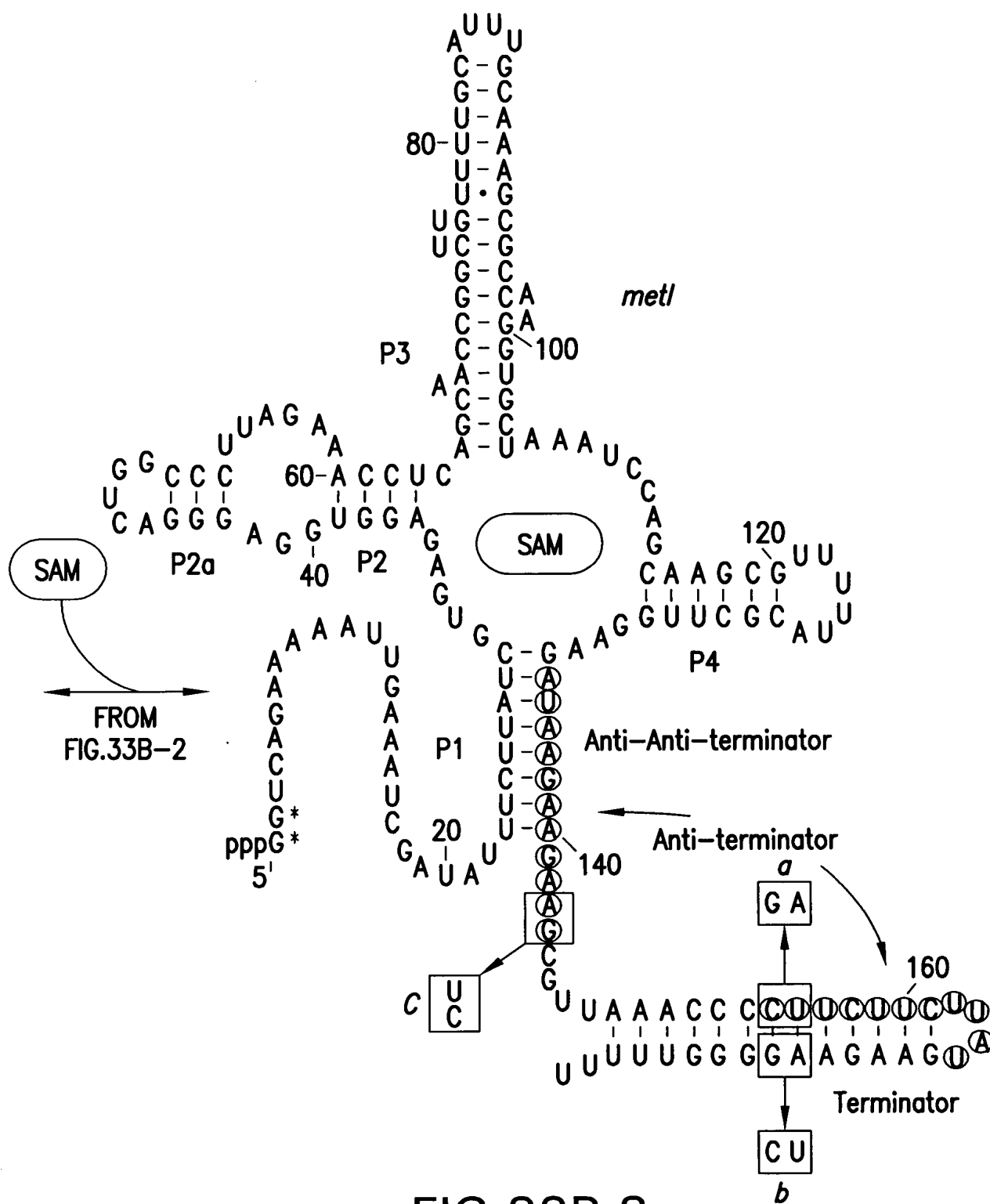




FIG. 34A

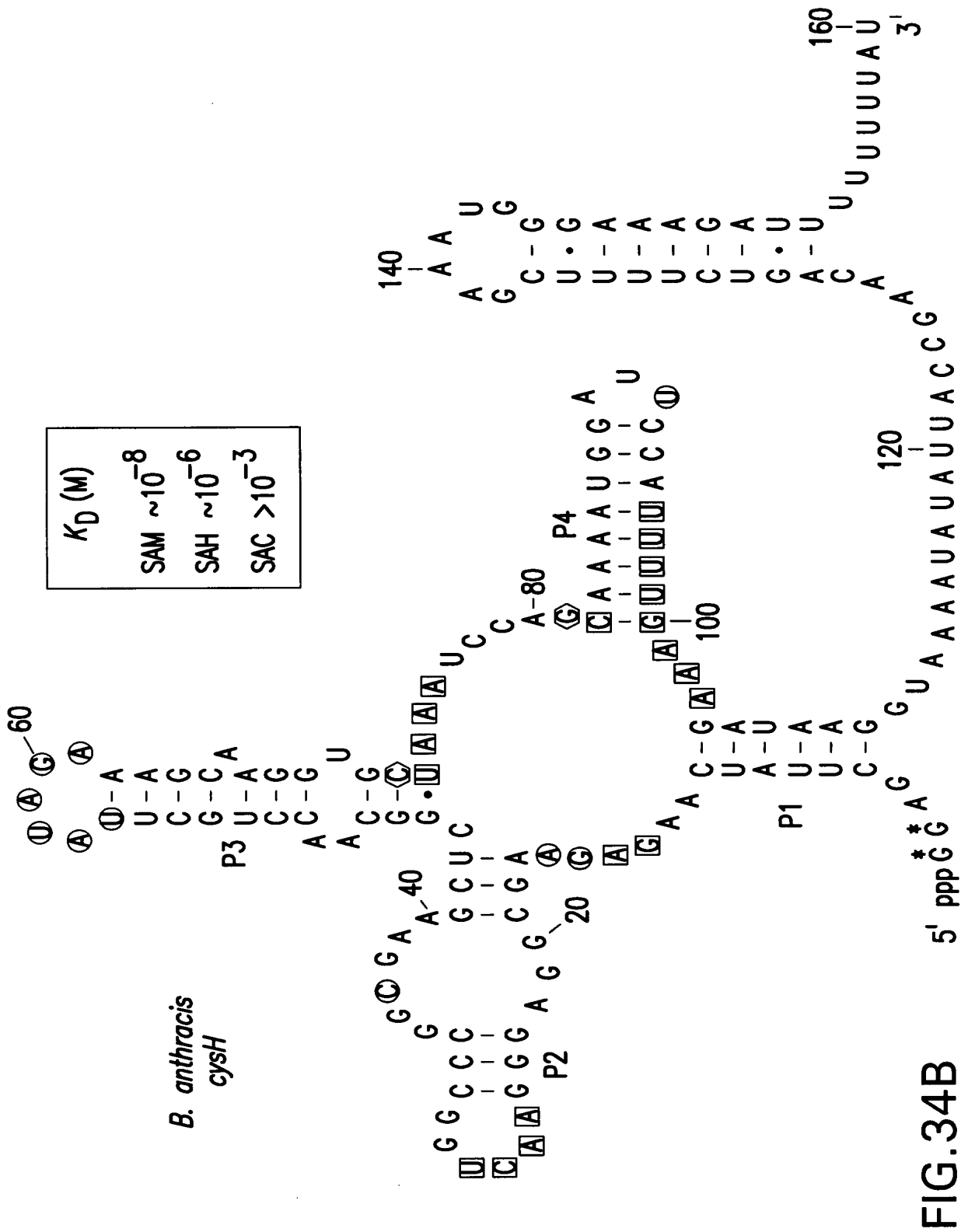


FIG.34B

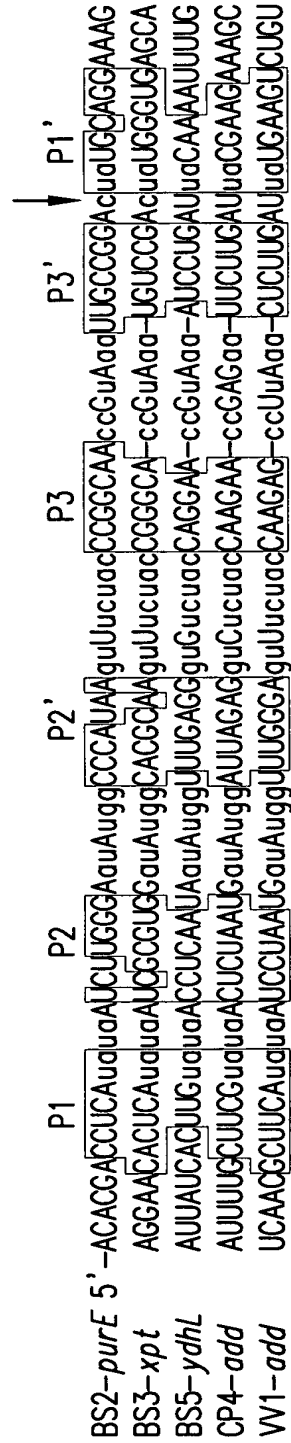


FIG.35A

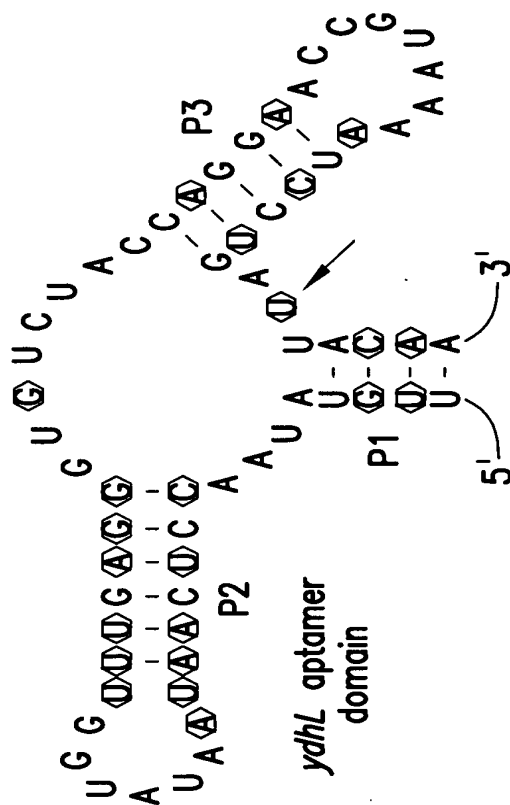


FIG. 35C

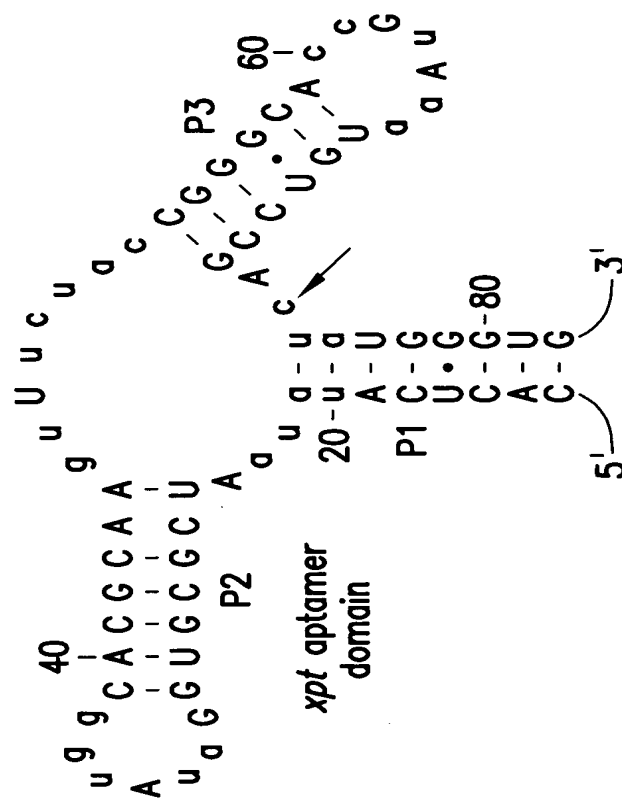


FIG. 35B

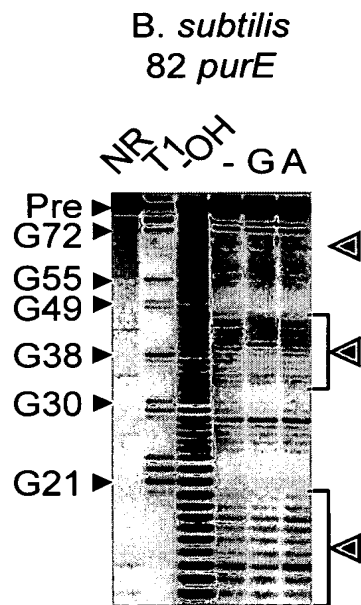


FIG.36A

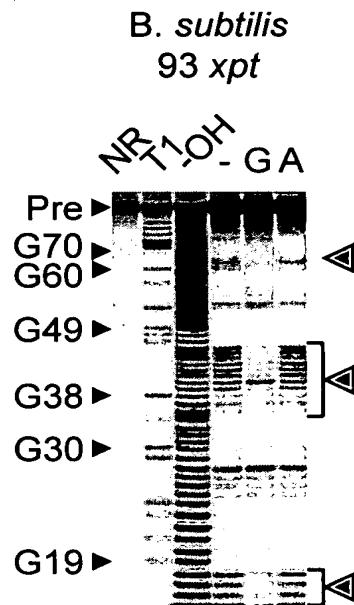


FIG.36B

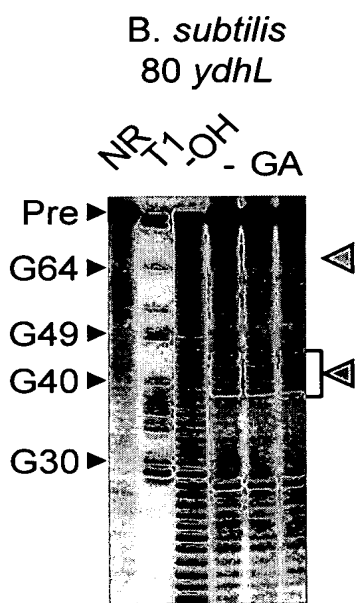


FIG.36C

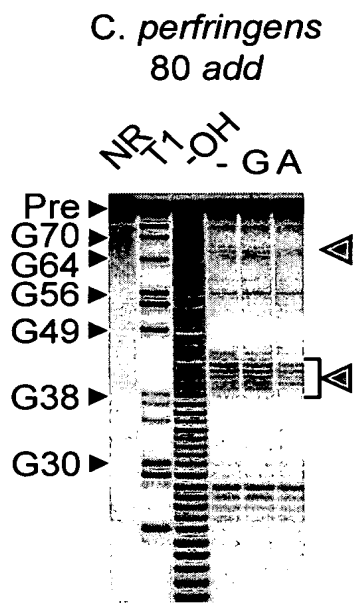


FIG.36D

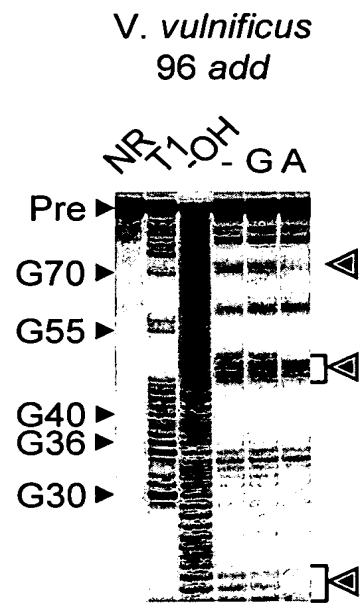


FIG.36E

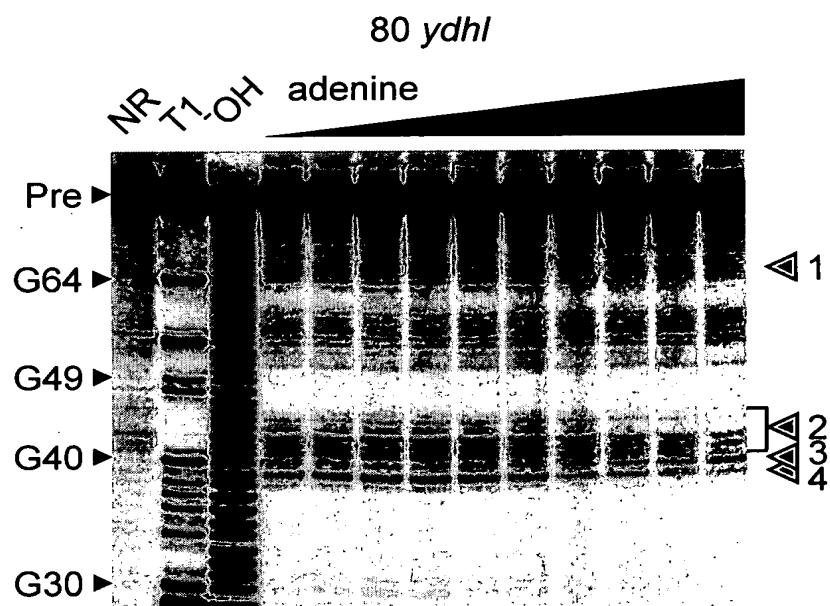


FIG.37A

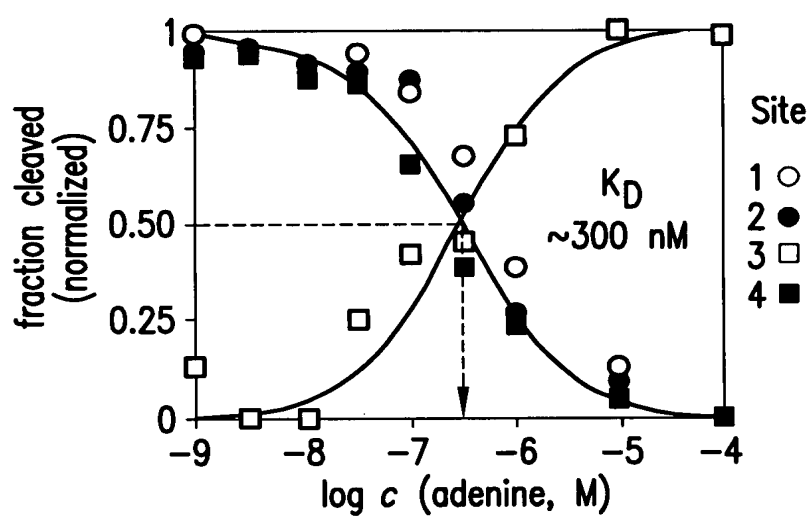


FIG. 37B

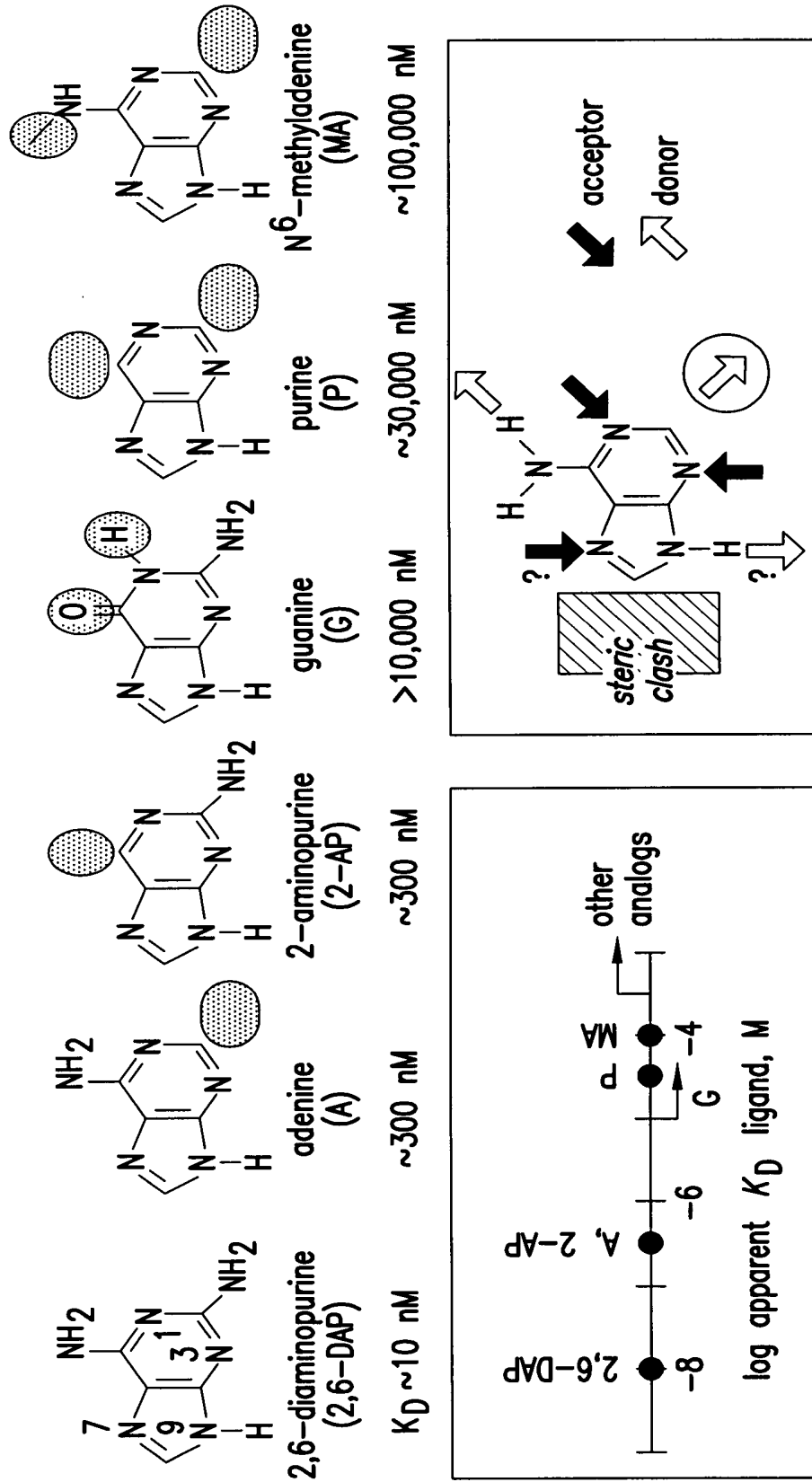


FIG.38A

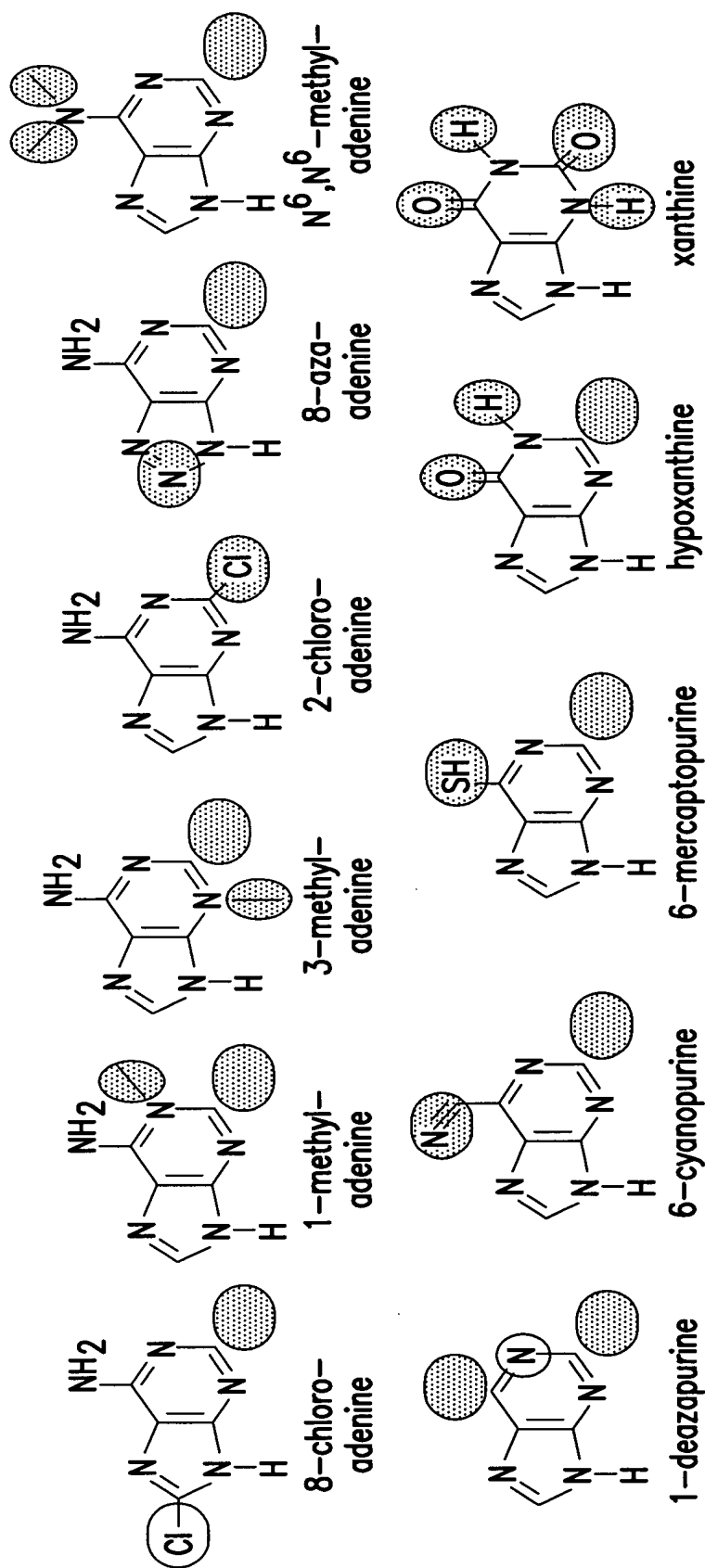


FIG. 38B

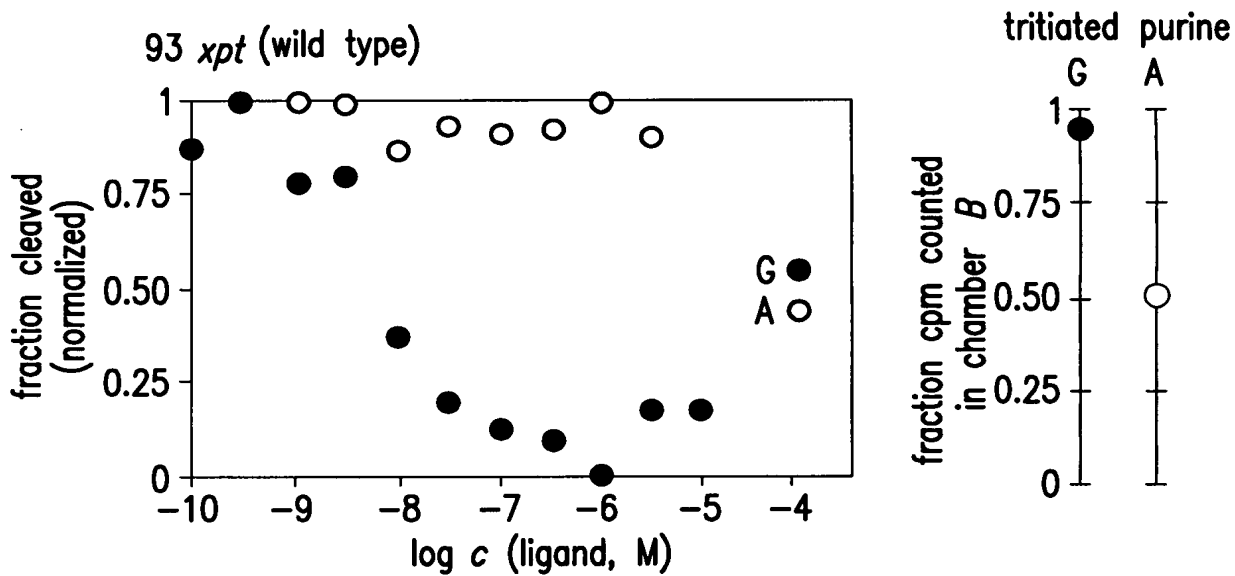


FIG. 39A

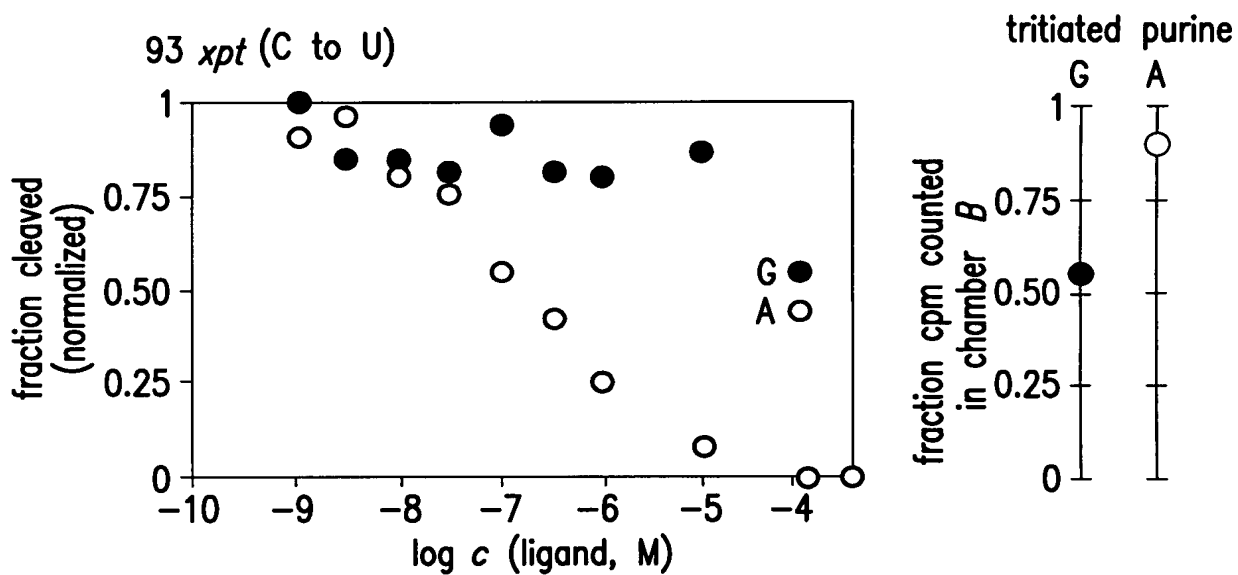


FIG. 39B

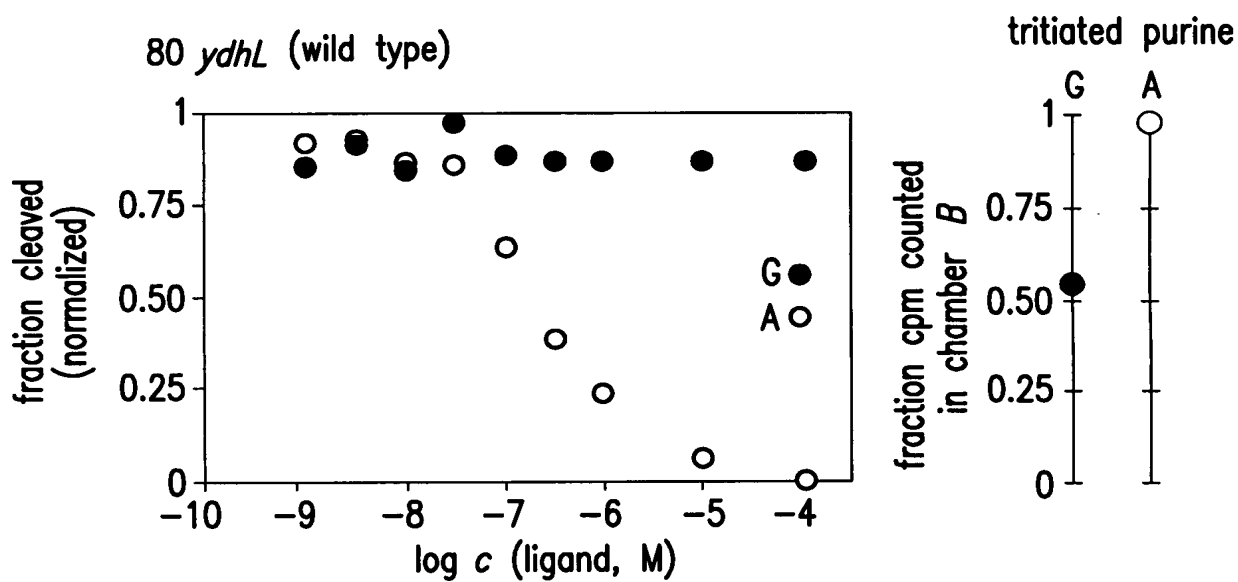


FIG. 39C

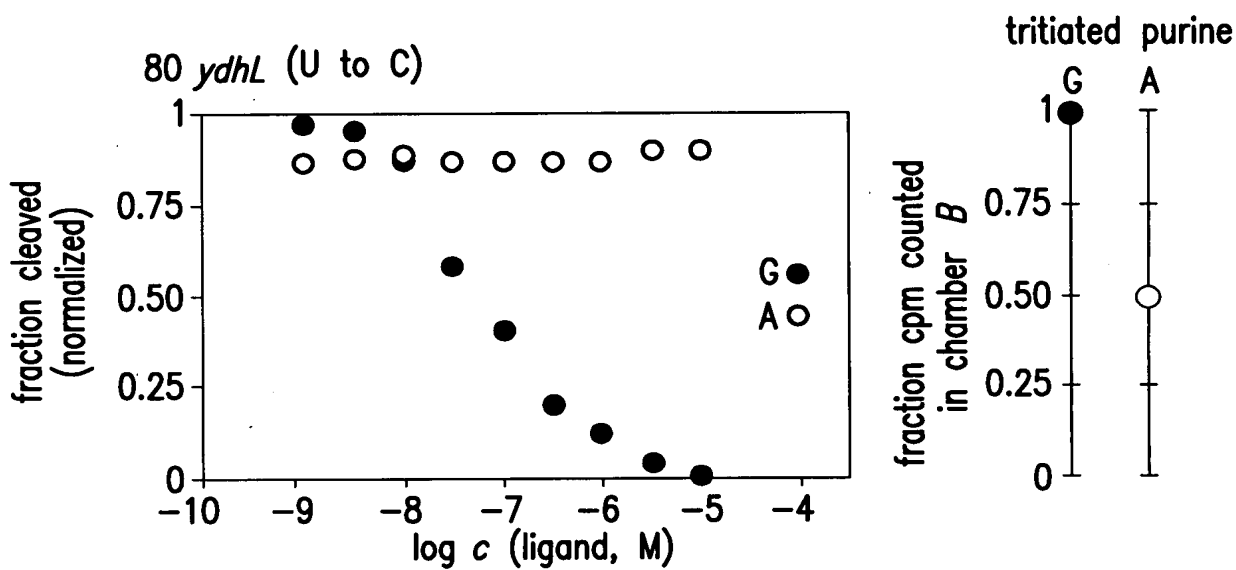


FIG. 39D

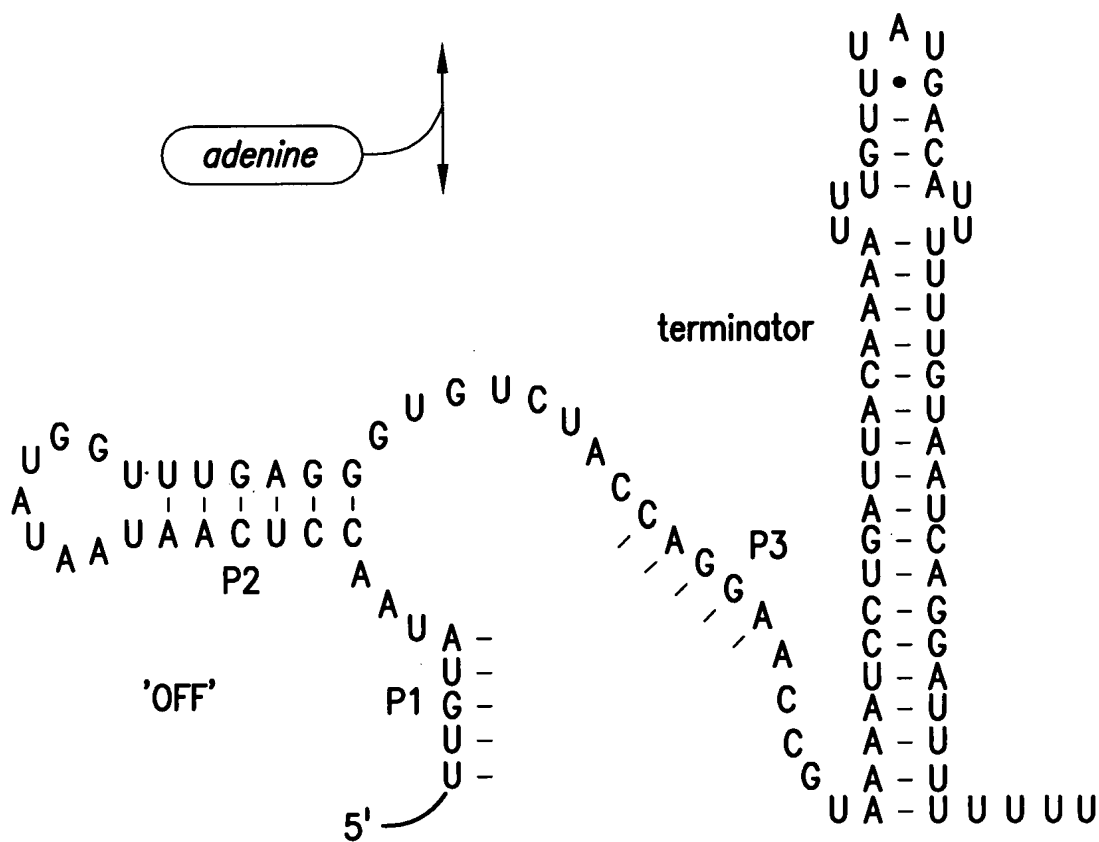
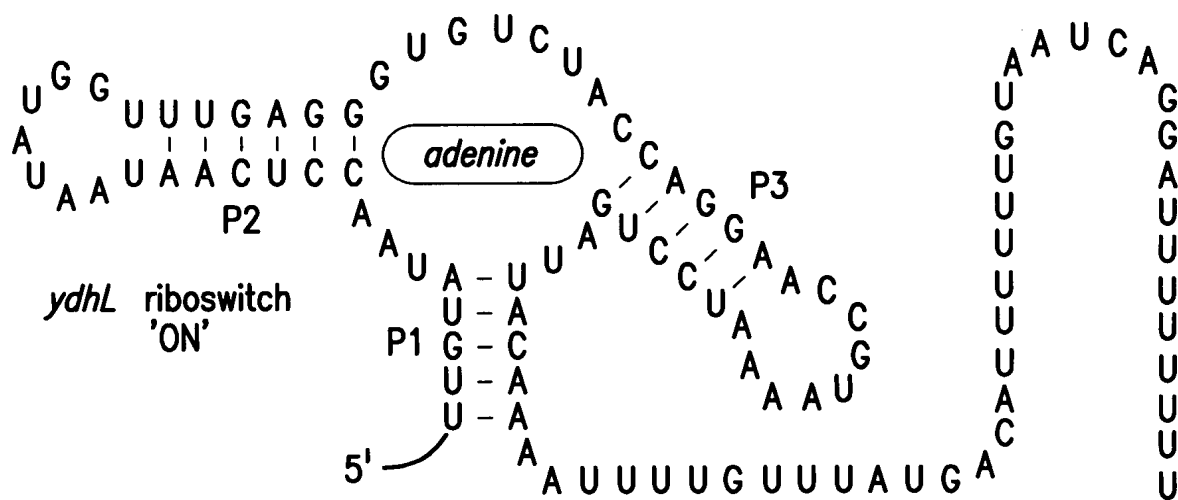


FIG.40A

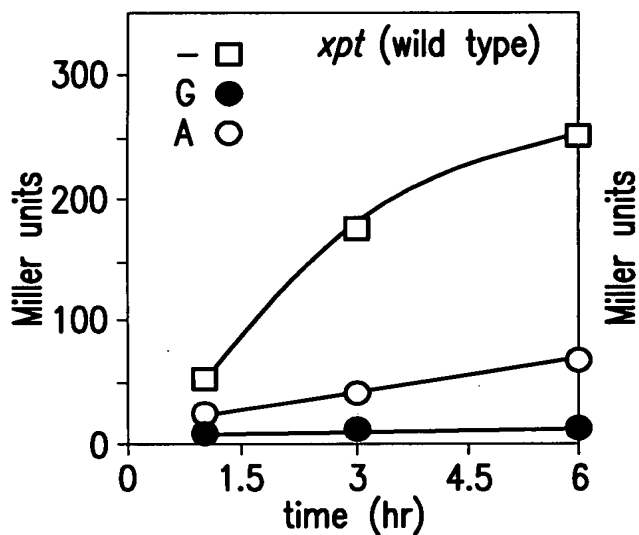


FIG. 40B

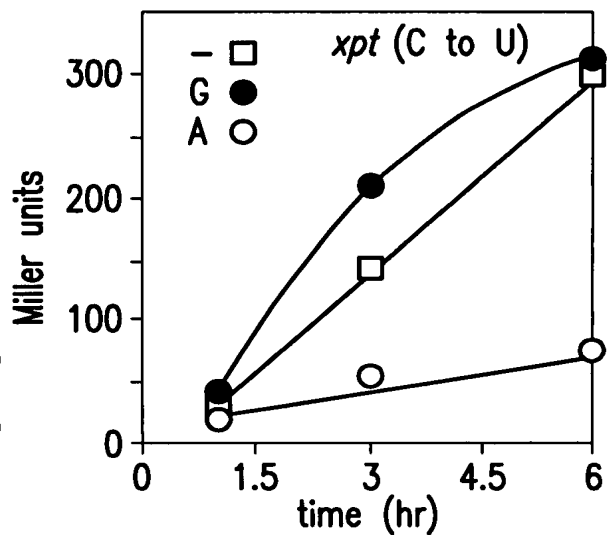


FIG. 40C

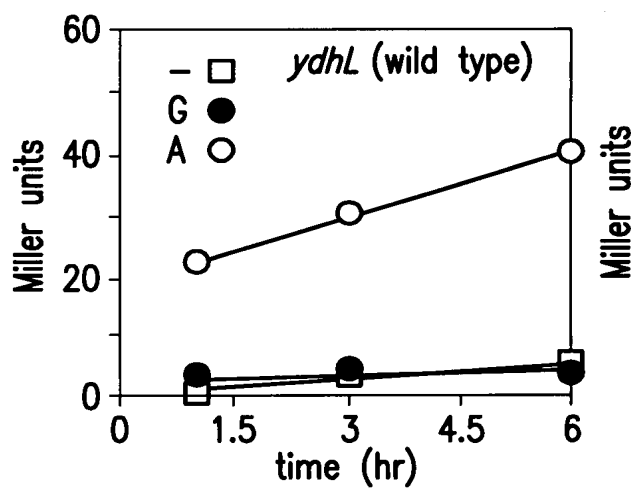


FIG. 40D

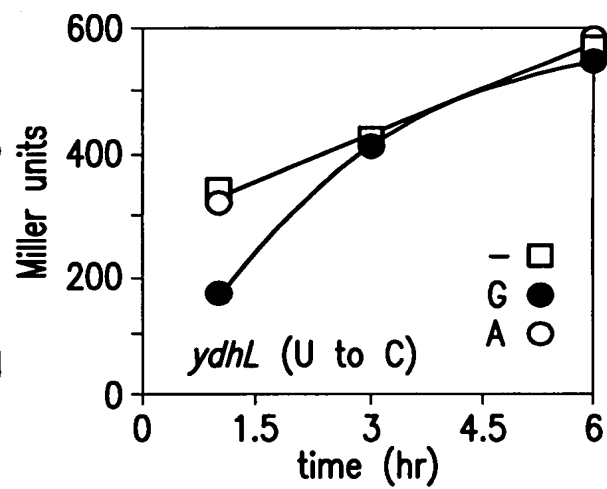


FIG. 40E

A. Alignment of SAM Riboswitches.

Table S1. S Box Sequence Alignment

ID	Position	Genbank Acc.	Organism	Remark	Start	Operon
Bs01	-	1180274	NC_000964.1	Bacillus subtilis	92	metF (yitJ)
Bs02	+	1257777	NC_000964.1	Bacillus subtilis	70	metB-metC (yjcI)
Bs03	-	1385353	NC_000964.1	Bacillus subtilis	130	metE (metC)
Bs04	-	1424147	NC_000964.1	Bacillus subtilis	89	ykrT-GCN3 (ykrT)
Bs05	+	1426344	NC_000964.1	Bacillus subtilis	60	rbcl-ykrX-araD-ykrZ (ykrW)
Bs06	+	1629516	NC_000964.1	Bacillus subtilis	164	cysH-pitA-MET3-cysC (cysH)
Bs07	-	2024504	NC_000964.1	Bacillus subtilis	86	ldhA-xy1B (yodD)
Bs08	-	3128412	NC_000964.1	Bacillus subtilis	170	metK (metE)
Bs09	-	3363560	NC_000964.1	Bacillus subtilis	108	abc -2011-nlpA (yusC)
Bs10	+	3996569	NC_000964.1	Bacillus subtilis	85	metE (yxiH)
Bs11	+	3997959	NC_000964.1	Bacillus subtilis	80	metE (yxiG)
Bh01	-	910190	NC_002570.1	Bacillus halodurans	141	???
Bh02	+	1348818	NC_002570.1	Bacillus halodurans	99	thrA
Bh03	+	1699959	NC_002570.1	Bacillus halodurans	175	metB-metC-metF-methH

FIG.41-1

Bh04	-	3427466	NC_002570.1	Bacillus halodurans	157	metK
Bh05	-	3591166	NC_002570.1	Bacillus halodurans	220	abc -2011-nlpA
Oi01	+	727028	NC_004193.1	Oceanobacillus iheyensis	78	meth
Oi02	-	1098097	NC_004193.1	Oceanobacillus iheyensis	162	metE
Oi03	+	1319043	NC_004193.1	Oceanobacillus iheyensis	76	???
Oi04	-	2134364	NC_004193.1	Oceanobacillus iheyensis	56	abc -???-nlpA
Oi05	-	2365511	NC_004193.1	Oceanobacillus iheyensis	176	metK
Oi06	-	2437305	NC_004193.1	Oceanobacillus iheyensis	129	abc -???-nlpA
Oi07	-	2708643	NC_004193.1	Oceanobacillus iheyensis	177	tran-MET17
Oi10	-	3200636	NC_004193.1	Oceanobacillus iheyensis	81	???-???
Oi08	-	2856863	NC_004193.1	Oceanobacillus iheyensis	201	???-???
Oi09	+	3162075	NC_004193.1	Oceanobacillus iheyensis	105	MET17
Oi10	-	3200636	NC_004193.1	Oceanobacillus iheyensis	81	???-???
Oi11	+	3200766	NC_004193.1	Oceanobacillus iheyensis	94	???
Oi12	+	3294474	NC_004193.1	Oceanobacillus iheyensis	97	abc-2011-nlpA-abgB
Oi13	-	3466518	NC_004193.1	Oceanobacillus iheyensis	112	gldA-nlpA-abc-2011
Ca01	+	453565	NC_003030.1	Clostridium acetobutylicum	78	metB-metC
Ca02	-	671354	NC_003030.1	Clostridium acetobutylicum	77	meth
Ca03	-	1073886	NC_003030.1	Clostridium acetobutylicum		(smtA-metB-cysK)
Ca04	+	1131539	NC_003030.1	Clostridium acetobutylicum	81	abc-2011-nlpA

(1)

(2)

FIG.41-2

Ca05	+	1976373	NC_003030.1	Clostridium acetobutylicum						102	metA
Ca06	-	2914839	NC_003030.1	Clostridium acetobutylicum						117	CAC5
Ca07	-	2991405	NC_003030.1	Clostridium acetobutylicum						70	metK
Cp01	-	2500081	NC_003366.1	Clostridium perfringens						391	metK
Cp02	-	2665229	NC_003366.1	Clostridium perfringens						102	rhaC
Lm01	+	137135	NC_003210.1	Listeria monocytogenes						90	oppA-dppB-dppC
Lm02	-	309383	NC_003210.1	Listeria monocytogenes						113	nlpA-abc-2011
Lm03	-	637924	NC_003210.1	Listeria monocytogenes						111	MET17-MET2
Lm04	+	882772	NC_003210.1	Listeria monocytogenes						97	metE
Lm05	-	1716649	NC_003210.1	Listeria monocytogenes						110	metK
Lm06	-	1739595	NC_003210.1	Listeria monocytogenes						109	metE-metB-metC-metH
Lm07	-	2491174	NC_003210.1	Listeria monocytogenes						93	abc-2011-nlpA
Li01	+	172401	NC_003212.1	Listeria innocua	(*)					88	oppA-dppB-dppC
Li02	-	327333	NC_003212.1	Listeria innocua	(*)					113	nlpA-abc-2011
Li03	-	636911	NC_003212.1	Listeria innocua	(*)					111	met17-met2
Li04	+	871751	NC_003212.1	Listeria innocua	(*)					97	metE
Li05	-	1772459	NC_003212.1	Listeria innocua	(*)					110	metK
Li06	-	1790189	NC_003212.1	Listeria innocua	(*)					109	metE-metB-metC-metH
Li07	-	2538251	NC_003212.1	Listeria innocua	(*)					92	abc-2011-nlpA
Sa01	+	15958	NC_002745.1	Staphylococcus aureus						41	met2

FIG.41-3

Sa02	+	875385	NC_002745.1	Staphylococcus aureus	91	abc-2011-nlpA
Sa03	-	1844603	NC_002745.1	Staphylococcus aureus	108	metK
Sa04	-	2381620	NC_002745.1	Staphylococcus aureus	13	rhaC
Sc01	+	4708438	NC_003888.1	Streptomyces coelicolor	26	thrC-moaD

FIG.41-4

ID	Position	Genbank Acc.	Organism	Remark	Start	Operon
Ct01	+	606192	AE_006470	Chlorobium tepidum	107	CAC5-MET2
Tt01	+	500245	NC_003869.1	Thermoanaerobacter tengcongensis	55	metK
Tt02	-	1750367	NC_003869.1	Thermoanaerobacter tengcongensis	66	metF-metH-ebcC
Tt03	-	2076680	NC_003869.1	Thermoanaerobacter tengcongensis	78	thrA-CAC5
Fn01	-	987483	NC_003454.1	Fusobacterium nucleatum	84	metK
Fn02	-	1317650	NC_003454.1	Fusobacterium nucleatum	91	abc-2011-nlpA
Dr01	+	1363063	NC_001263.1	Deinococcus radiodurans, chr 1	156	abc-2011-nlpA-nlpA
Dr02	+	980704	NC_001263.1	Deinococcus radiodurans, chr 1	41	metH-???-metF
Xa01	-	3558018	NC_003919.1	Xanthomonas axonopodis	74	MET2-metC-thrA
Xc01	-	3379769	NC_003902.1	Xanthomonas campestris	73	MET2-metC-thrA
Se01	+	574	AF_269983.1	Staphylococcus epidermidis genomic clone		
Se02	-	142	AF_270301.1	Staphylococcus epidermidis genomic clone		
Gs01	+	342843	contig:2947	Geobacter sulferreducens		
Gs02	+	2470946	contig:2947	Geobacter sulferreducens		
Ba01	-	177272	contig:6615	Bacillus anthracis		
Ba02	+	185586	contig:6615	Bacillus anthracis		
Ba03	-	197185	contig:6615	Bacillus anthracis		
Ba04	+	320607	contig:6615	Bacillus anthracis		

FIG.41-5

Ba05	-	371127	contig:6615	Bacillus anthracis	(*)
Ba06	+	1362659	contig:6615	Bacillus anthracis	
Ba07	+	1375353	contig:6615	Bacillus anthracis	
Ba08	+	2459362	contig:6615	Bacillus anthracis	
Ba09	-	2953226	contig:6615	Bacillus anthracis	
Ba10	-	3091676	contig:6615	Bacillus anthracis	
Ba11	-	3890736	contig:6615	Bacillus anthracis	
Ba12	+	3892933	contig:6615	Bacillus anthracis	
Ba13	+	4074285	contig:6615	Bacillus anthracis	
Ba14	-	4074078	contig:6615	Bacillus anthracis	
Ba15	-	4553682	contig:6615	Bacillus anthracis	
Ba16	-	4739975	contig:6615	Bacillus anthracis	
Ba17	-	5140322	contig:6615	Bacillus anthracis	
Bc01	+	26115	contig:1617	Bacillus anthracis	(*)
Bc02	+	748841	contig:1617	Bacillus cereus	
Bc03	+	1183078	contig:1617	Bacillus cereus	(*)
Bc04	+	1195849	contig:1617	Bacillus cereus	(*)
Bc05	+	2200884	contig:1617	Bacillus cereus	(*)
Bc06	-	2684484	contig:1617	Bacillus cereus	(*)
Bc07	-	2963724	contig:1617	Bacillus cereus	(*)

FIG.41-6

Bc08	-	2773209	contig:1617	Bacillus cereus	(*)
Bc09	+	3500608	contig:1617	Bacillus cereus	(*)
Bc10	-	3687209	contig:1617	Bacillus cereus	(*)
Bc11	+	3687417	contig:1617	Bacillus cereus	(*)
Bc12	-	3498410	contig:1617	Bacillus cereus	(*)
Bc13	-	4205859	contig:1617	Bacillus cereus	(*)
Bc14	-	4397125	contig:1617	Bacillus cereus	(*)
Bc15	-	4784934	contig:1617	Bacillus cereus	(*)
Bc16	-	5114094	contig:1617	Bacillus cereus	(*)
Bc17	-	5094322	contig:1617	Bacillus cereus	(*)
Bc18	+	5101784	contig:1617	Bacillus cereus	(*)

FIG.41-7

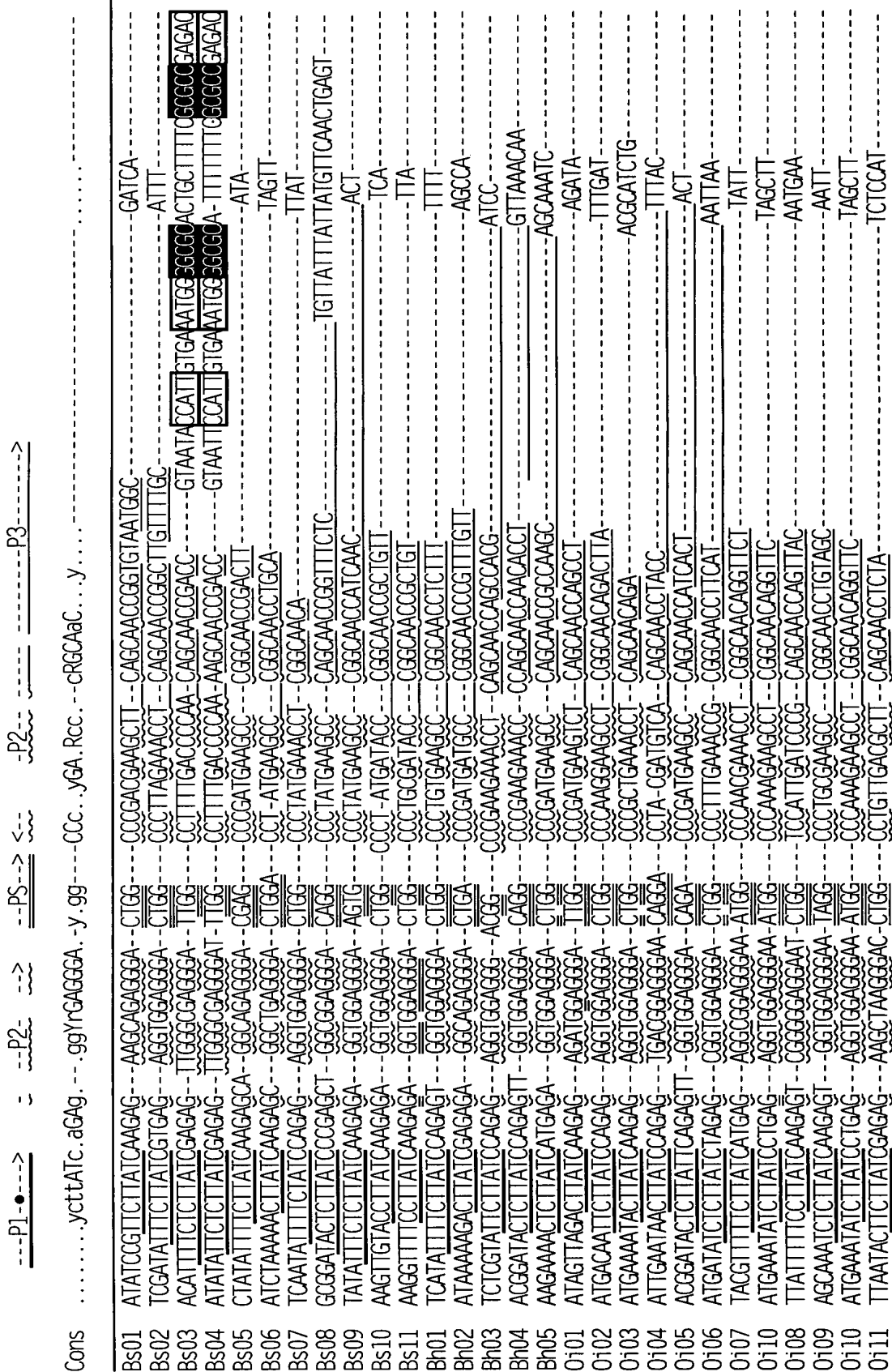


FIG.41-8

Oi12 ACCTTTTCTTCTATGAG--AGATTGAGGGAT-CAGG--CCCTATGACAICI--CGGCAGCGGATCTTTA-----TAT-----
 Oi13 CTAATATCTCTTATGAGAGT--GGCTGAGGGA--CTGG--CCCTGTAGGCC--CGGCAACCGTTTCATCGT-----AATCCCA-----
 Ca01 TAAATTGTTCTTATCAAGAGT--GACGGAGGGA--TAGG--CCCTATGAGTC--CGGCAACATCCAA-----TTATT-----
 Ca02 TGTAAATCTTATCAAGAGT--GGTGGAGGGA--CTGG--CCCTTTGAACC--CGGCAACCGATATATT-----TTT-----
 Ca03 TAATATTCTTATCAAGAGT--AAACGGAGGGA--CTGG--CCCAATGATGTTI--CAGCAACCAAGGT-----TTTAT-----
 Ca04 ATTAGTGCACCTTATCAAGAGA--GGTGGAGGGA--CCGG--CCCTGTGAAGCC--CAGCAACCTGTATA-----TGTTAAT-----
 Ca05 ATATTATTCTTATCAAGAA--GGTGGAGGGA--CTGG--CCCTATGAAGCC--TGACAAACCGGC-----AAAT-----
 Ca06 TGATAAGGCTTATCAAGAGA--GGTGGAGGGA--CTGG--CCCTATGAACC--CAACAACCGCATTTI-----TTTAATT-----
 Ca07 ATGGAACCTTATCAAGAGA--GGTGGAGGGA--AGGG--CCGTTGAACC--CGGCAACCGATGTTAT-----AATTAA-----
 Cp01 TTATATACCTTATCAAGAGA--GGTGGAGGGA--AAGG--CCCTATGAACC--CGGCAACCGATGA-----GAAA-----
 Cp02 TTAATAAATCTTATCAAGAGA--GGTGGAGGGA--CTGG--CCCTGTGAACC--CAGCAACCGGTAAITCTTTGGCGTTAAACAAATGCTGATTTTAAATATAAAAAATCAGTAGTA
 Lm01 TTACGTTTCTTATCAAGAGT--GGTGGAGGGA--ATCGG--CCCACTGAACC--CAGCAGCGGAGC-----GCAA-----
 Lm02 ATATTCTCTTATGAGAGC--GGCAGAGGGA--CTGG--CCCGATGAAGCC--CGGCAACCTAGCTTTAT-----TTAAGC-----
 Lm03 TAGTATTTCTTATCAAGAA--AGGTGGAGGGA--CTGG--CCCTTTGAAGCC--TAGCAACCGGAA-----TTTAT-----
 Lm04 ACATAGTAACCTTATCAAGAA--AGGTGGAGGGA--CTGG--CCCGTGAAGCC--TGGCAACCGGA-----TTT-----
 Lm05 AATTATCTTATCAAGAGC--GGTAGAGGGA--CTGA--CCCTTTGAAGCC--CAGCAACCTACAC-----ATATAA-----
 Lm06 TAAATTGCTCTTATGATAGT--GGTAGAGGGA--CTGG--CCCGTTGAACC--CGGCAACCTTTCAA-----TACG-----
 Lm07 TGTAAGAACTTATCAAGAGT--GGTGGAGGGA--AATG--CCCTATGAAGCC--CAGCAACCTAAACAATAA-----TTCA-----
 Li01 TTACAAATCTTATCAAGAGT--GGTGGAGGGA--TCGG--CCCACTGAACC--CGGCAACCGGAGC-----GCAA-----
 Li02 ATATTCTCTTATGAGAGC--GGCAGAGGGA--CTGG--CCCGATGAAGCC--CGGCAACCTAGCTTTAT-----TTAAGC-----
 Li03 TAGTATTTCTTATCAAGAA--AGGTGGAGGGA--CTGG--CCCTTTGAAGCC--TAGCAACCGGAA-----TTTATT-----
 Li04 ACATAGTAACCTTATCAAGAA--AGGTGGAGGGA--CTGG--CCCACTGAAGCC--TGGCAACCGGA-----CTTT-----
 Li05 AATTATCTTATCAAGAGC--GGTAGAGGGA--CTGA--CCCTTTGAAGCC--CAGCAACCTACAC-----ATATAA-----
 Li06 TAAATTACTCTTATGATAGT--GGTAGAGGGA--CTGG--CCCGTTGAACC--CAGCAACCTTTCAA-----TTCG-----
 Li07 TGTAAGAACTTATCAAGAGT--GGTGGAGGGA--AATG--CCCTGTGAACC--CAGCAACCTAAACAATAA-----TTCA-----
 Sa01 TTCATATTCTTATGAG--AAGTTGAGGGA--TTGG--CCCTGTGATCTI--CAGCAACCGACT-----TTAT-----
 Sa02 CGGTAAATCTTATCAAGAGT--GGTGGAGGGA--TTGG--CCCTACGAGCC--CGGCAACCGCTI-----ATATA-----
 Sa03 ACGGATTCTTATCTGAGT--GGTGGAGGGA--ATGG--ACCAATGAACC--CAGCAACCTCTTTI-----TTTAT-----
 Sa04 TAAGCATCACTTATGAG--AGGTGGAGGGA--CTGG--CCCTATGAAGCC--CGGCAACAT-----CTGA-----
 Sc01 TTCATACCGCTATCAAG--GGCAGAGGGAT--ACGG--CCCGATGAAGGCC--CGGCAACCTCCAGTCGG--TCTTGTGACACAGGACGTGGCGAGGCTC--

FIG. 41-9

	---P1--->	~	--P2-->	--PS-->	<--	-P2--	-----P3----->
ConsycttATc.aGAg.--	ggYrGAGGGA.y.gg	CCc.yGA.Rcc.--cRGCAaC...y.....				
Ct01	TTTCAGCTATCATCCAGAA--	AGGCGGAGGGA--CTGG	CCCTGCGAAGCCT--	TGGCAACCTTCAT--			TCCAC--
Tt01	TAACACGCCTTATCAAGAGA--	GGTGGAGGGA--AGAG	CCCGATGAACC--	CGGCAACCTGTCT--			TTTAA--
Tt02	TTAAATCTCTATCAAGAGA--	GGTGGAGGGA--CTGG	CCCGATGAACC--	CGGCAACCTAGC--			TTAG--
Tt03	CTCAATCCTCTATCAAGAGT--	GGTGGAGGGA--CTGG	CCCGATGAACC--	CGGCAACCTAGC--			GTA--
Fr01	TGGAATAAACCATCAAGAG--	AGATTGAGGGA--CAGG	CCCGTTGAGATCT--	CAGCAACCTAGC--			TAAAA--
Fr02	AAATAAATAACCATCAAGAG--	AAACGGAGGGA--CTGG	CCCAATGATGTT--	CAGCAACCTAGC--			TTAAAT--
Dr01	AGGTCACCTTATCCAGAGT--	CGCGCAGGGA--CTGG	CCCATGACCGCG--	CAGCAACCTAGC--			CTCATCAC--
Dr02	CGGTGGGGTATCCAGAGT--	CGGCCAGGGTG--TTCTG	CCCGCCTAGGGG--	CAGCAACCTAGC--			TTCATCAC--
Xa01	CCTAGCCTCACCATCGAGC--	CGCGGAGGGA--CAGG	CCCTTTGATGCG--	GGGCAACCTAGC--			GCAA--
Xc01	CGTAGCCTCACCATCGAGC--	CGCGGAGGGA--CAGG	CCCTTTGATGCG--	GGGCAACCTAGC--			GCAA--
Se01	TTACCTAACCTTATTTAG--	AAGCTAGGGAT--TTGG	CCCATAGAGCTT--	CAGCAACCTAGC--			TTAAAT--
Se02	ACGGATCTCTATCTAGT--	GGTGGAGGGA--ATGG	ACCAATGAACC--	CAGCAACCTAGC--			ATTT--
Gs01	GTAGACCTTCTATCAAGAG--	TGGTGGAGGGA--AAGG	CCCTGTGAACCA--	CAGCAACCTAGC--			GTAG--
Gs02	ACGGCTTAACCTATCAAGAG--	CGACGAGGGA--CAGG	CCCGGTGAGTGG--	CGGCAACCTAGC--			ATGG--
Ba01	ACACATCTCTATCAAGAGT--	GGCGGAGGGA--CTGG	CCCGATGATGG--	CGGCAACCTAGC--			ACG--
Ba02	AGCAATTAACCTATCAAGAG--	AGGTAGAGGGA--CTGG	CCCTATGACCT--	CAGCAACCTAGC--			GTATA--
Ba03	TTTACTCATTTATCAAGAG--	AGGTGGAGGGA--CTGG	CCCTTTGAACCT--	CGGCAACCTAGC--			TTTT--
Ba04	CGATACATTTATCAAGAG--	AGGTGGAGGGA--CTGG	CCCTACGATACCT--	CAGCAACCTAGC--			TTTT--
Ba05	GAATAATCTTATCAAGAGA--	GGCAGAGGGA--CGGG	CCCTTTGAAGCC--	CAGCAACCTAGC--			ATAC--
Ba06	AATACAAGCTTATCAAGAGA--	AGCGGAGGGA--CTGG	CCCGCGGAGCT--	CGGCAACCTAGC--			ATAGA--
Ba07	TGAACCTTCTTATAAAGAG--	AGCGGAGGGA--CTGG	CCCTACGATGCT--	CGGCAACCTAGC--			GATTTTA--
Ba08	AAATTAATCTTATCAAGAG--	AGGTGGAGGGA--CGG	CCCTATGAACCT--	CAGCAACCTAGC--			AAAT--
Ba09	ATGAATTTCTTATCAAGAG--	AGGTGGAGGGA--CTGG	CCCTATGAACCT--	CGGCAACCTAGC--			TIA--
Ba10	GAATATTTCTTATCAAGAG--	GGTGGAGGGA--CTGG	CCCGATGAACC--	CAGCAACCTAGC--			GAT--
Ba11	TATACAACCTTATCAAGAGA--	GGTGGAGGGA--TTGG	CCCGATGAACC--	CAGCAACCTAGC--			GTATAACCATTTGTAATGGGGTTTATGACGGCA
Ba12	TAAATCTTCTTATCAAGAGA--	GGTGGAGGGA--CGAG	CCCGAGGAACC--	CGGCAACCTAGC--			TAAT--
Ba13	ACGAACATTTATCTAGAG--	AGGTAGAGGGA--CTGG	CCCTATGACCT--	CAGCAACCTAGC--			ATTT--
Ba14	AAGACAACCTTATCTAGAGC--	GGTGGAGGGA--AAGG	CCCTGTGAACC--	CGGCAACCTAGC--			GAAAT--

FIG.41-10

Ba15	GGATACTCTCTTATCCGAGCT--GGCGGAGGGA--CAGG--CCGATGAAGCC--CAGCAACCTCAGTTGTA--GTGGTAAA--
Ba16	CTGATTCTCTTATCAAGAGA--GGTGGAGGGAC--TGTG--CCCTGTGAAGCC--CGGCAACCGTCAAC--TTAT--
Ba17	TTGCATAGTCTTATCAAGAA--AGGTGGAGGGA--CAGG--CCCGATGAACCT--TGGCAACAGCGGT--ATA--
Bc01	CGATACATTCTTATCCAGAG--AGGTGGAGGGA--CTGG--CCCTACGATACCT--CAGCAACGGGT--TTTT--
Bc02	CAACAATTCTTATGTTAG--AGTGGAGGGA--CGGG--CCCTATGAACCT--CGGCAACCTCGT--ATGAG--
Bc03	AATACAAAGCTTATCAAGAGA--AGCGGAGGGA--CTGG--CCCGGCGAAGCT--CGGCAACCTGCT--ATAGA--
Bc04	TGAACCTCTTATTAAGAG--AGCGGAGGGA--CTGG--CCCTACGATGCT--CGGCAACCGGACTC--GATTCA--
Bc05	AAATTAACTTATCCAGAG--AGGTGGAGGGA--CGG--CCCTATGAACCT--CAGCAACCCCTATA--TATATT--
Bc06	ATGAAATCTTATCAGAG--AGGTGGAGGGA--CTGG--CCCTATGATACCT--CGGCAACCGGATTGG--TTA--
Bc07	ATTAGTTTCTTATTAAGAG--AGTGGAGGGA--CTGG--CCCGATGAATCT--CAGCAACAGGCT--ATAAA--
Bc08	GAATATTTCTTATCCAGAGA--GGTGGAGGGA--CTGG--CCCGATGAAGCC--CAGCAACCGC--GAT--
Bc09	TAAATACCTCTTATCAAGAGA--GGTGGAGGGA--CGAG--CCCGACGAAGCC--CGGCAACCGATCTAC--AATT--
Bc10	AGACAACTCTTATGAGAG--GGTGGAGGGA--AAGG--CCCTGTGAAGCC--CGGCAACCTTCAAC--GAAT--
Bc11	ACGAACATCTTATCTAGAG--AGGTAGAGGGA--CTGG--CCCTATGAGGCT--CAGCAACCATTAAC--ATTT--
Bc12	TATACACTCTTATCAAGAGA--GGTGGAGGGA--TTGG--CCCGATGAAGCC--CAGCAACCGACC--GTAATA--
Bc13	GGATACTCTCTTATCCGAGCT--GGCGGAGGGA--CAGG--CCCGATGAAGCC--CAGCAACCTCAGTTGT--TTATGTAAC--
Bc14	CTGATTCTCTTATCAAGAGA--GGTGGAGGGA--TGTG--CCCTGTGAAGCC--CGGCAACCGTCAAC--TTAT--
Bc15	TTGCATAGTCTTATCAAGAA--AGGTGGAGGGA--CAGG--CCCGATGAACCT--TGGCAACAGCGGT--ATA--
Bc16	TTTACTCATTTGATCAAGAG--AGGTGGAGGGA--CTGG--CCCTTGAACCT--CGGCAACCGGTTCA--TTTT--
Bc17	ACACATACTCTTATCAAGAGT--GGCGGAGGGA--CTGG--CCCGATGATGCC--CGGCAACCGAGCTTATA--ACG--
Bc18	AGCAATTACTTATCCAGAG--AGGTAGAGGGA--CTGG--CCCTATGACACCT--CAGCAACCGGTTCT--GTAATA--

FIG.41-11

Cons	<-----P3-----<PS-r.GTGYaa.t-Cc.r.....	---P4--> carr.....	<-P4---<---*-P1--yytgrraGATRagrr.rr.....
Bs01	GCATGACCAAGGTGCTAAAT-CCAG	CAAGCT	GCITGGAAGATAAGAGAGACAAAATCACTGACAAA
Bs02	GCAAGGCGCAAGGTGCTAAAT-CCAG	CAAGCGT	ATGCTTGGAGAGATAAGAAAGCGTTAAA
Bs03	TGATGTCTCATAA	CAGAT	GTCGAGAGATGAGAGAGCGAGTGTTCAGTAGAAAA
Bs04	GCTGTCTCTTAA	T-CAGAT	ATCTGAGAGATAAGAGAGCGGACATAGATGTTAA
Bs05	AAGCAGCGGTGCTAAAT-CTTG	CAGCT	GGCTGAGAGATAGATTCGGACGAGAACGAAA
Bs06	TGTAAAGGTGCT-ACITCCAG	CAAAATG	CATTTTGAAGATAAGGGCTGCATGCTGTTCTGT
Bs07	IGTGCCAAAT-CCAG	CAAGC	GCITGGAAGATAGGAAGCAAGGTTTATACGGCGTCTGCCTG
Bs08	GAGACAACCAAGGTGCTAA-CCTG	TTGCAAGG	CCITGAGCGATAAGAGTGAAGGACAAAGACCAAA
Bs09	GTTGAATGGTGCCAAAT-CACT	CGAAGC	GCITTGAAGATGAGAGAAAGGCATTTTATATAA
Bs10	AACAGAAATGGTGTAAAT-CTT	AAGAAC	GTCTTTCGAGATGAGGGGAGATTTGATGTTCAA
Bs11	ACAGAAATGGTGTAAAT-CTT	TAGAGCAA	TTGCTCTTGAAGATAAGGTTGAGATGTCAGGCAA
Bh01	AAAGAGGTGCCAAT-CCAG	CAGAAC	GTCTTGAAGATAAGAAAGCGAAGCGGATCG
Bh02	AGCAACCAAGGTGCTAAAT-TCAG	CAGATG	CATTCTGGAAGATAAGCGAAGCGGCAAAA
Bh03	IGTGGTCAGGTGCTAAAT-CCTG	CAAGCA	IGCTTGAGAGATAAGAGGAAGCGAGTGAGATCCAA
Bh04	AGGTGAAGGTGCTAA-CCTG	CAAGCC	GCCTTGAAGATAAGAGCGGAAAGGTATGTTAATTAA
Bh05	GCITGGAAAGGTGCTAAAT-CCTG	CAAGC	GCITTGAGAGATGAGAGAAAGGGAAGAGTAAACATT
Oi01	AGGTATGGTGTAAAT-CCAA	TAGGCT	AGCCTTAAAGATAAGAGAGCTATGTTATTAA
Oi02	TAAGTACITGGCCAAAT-CCAG	TAGCG	TGCTAGAAGATGAGAAAGAGTATATAGTACGGTTCTCTGTA
Oi03	TCITGTCTAAAT-CCTG	CAAGC	GCITGGAAGATAAGTTGAGGTATCGTAATATCCAAGTCTCT
Oi04	GGAGTGGTGT-TCITCTTG	CAGAA	TTCTGAAAGATAAGGTAAATGATATGTAATAA
Oi05	GGTGAAGGTGCTAA-TCTG	ATGCAAGGA	TCCTTGAACCAATAAGAGCGGAAGGCCATAATTCTT
Oi06	ATGAAGGTGCCAAAT-CCTG	CA	IGAAAGATGAGAGAACGTCAGAGGATATACGATAAATAAG
Oi07	AGAATACTGTGCCAAT-CCAT	CAAGCA	TGCTTGAAGATAAGAGTAGAATAATTTATAGCTTTAAAA
Oi10	GAATACTGTGCCAAT-CCAT	CAAGTAT	ATGCTTGGTAGATAAGAGAAAGTCGCGGACAGAG
Oi08	GTAACATGGTGTCAAT-CCAG	CAAGC	GCITGATAGATGAGAAAAGTGTATACCTTTTAAATAAAA
Oi09	GCTATGAAGGTGCTAAAT-CCTA	CAGAC	GTCTGGAAGATAAGAGGAGGTTCGGTTTAAACAGACAAA
Oi10	GAATACTGTGCCAAT-CCAT	CAAGTAT	ATGCTTGGTAGATAAGAGAAAGTCGCGGACAGAG
Oi11	TAGAAGGTGTACCT-CCAG	CAAGAT	GTCTTGAAGATAAGAGTCCAGATTAAAAAAA

FIG. 41-12

0i12	-----TAAAGTA	CTGTGCCAAT	-CCTG	-----CAAATGC	-----AAACGA	-----GCATTGAAAGATGAGAAACGATGGCTTACATATATACATATG
0i13	-----GTGATGAAT	AGGTGCTAAAT	-CCTG	-----CAAAATAC	-----GGACA	-----GTATTTGAGAAATAAGAGAGGTGATGAATGACTTACGTAGTGTA
Ca01	-----TTGGAGAT	GTCTAAT	-CCTA	-----CAGG	-----TTAT	-----CCTGAGAGATGAGAAATGTTTTTAAAA
Ca02	-----AATATAT	GTGGTCAAT	-CCTG	-----CAGC	-----AAAC	-----GCTGATAGATGAGAAATATTCGCGAATGTAAA
Ca03	-----ACTATAT	GTGGTCAAT	-CCAG	-----CAGGA	-----TATT	-----TTCTGAAAGATGAGGAGCGACTATTTAAACATTTTTATTGT
Ca04	-----TATACAGG	TGCTAAT	-CCTG	-----CAGC	-----GCTA	-----GCTGAGAGATGAGAAATATAAATCGAGCTTTTA
Ca05	-----GTACGGT	TTAAT	-CCTG	-----CAAAAC	-----TTATTT	-----GTTTTGAAAGATAAGAAAAACAGCTTATTAATTAATGAGTATGTT
Ca06	-----AGATGAT	GTGGTCAAT	-CCTG	-----CAAG	-----TTAA	-----TTTTGAGAGATAAGAGGATTATAAATTTTAGAAAGCTAAAA
Ca07	-----AGTACATA	TATGGTCCAAAT	-CCTG	-----CAGAA	-----TTA	-----TTCTGCAAGATAAGAGAGAGAAATGTAA
Cp01	-----TCACTACGG	TGCCAAT	-CCGG	-----TAAAGA	-----AAT	-----TCTTTACAAGATGAGAGAAAGATAAATTTAGTGTATAACTAAAA
Cp02	-----TTATAGCGG	TGCTAAT	-CCTG	-----CCGT	-----AGAA	-----ACTGAGAGATAAGAAAGAGAGTCTGTAAAGAAATAATA
Lm01	-----GTTCTAT	GTCTAAT	-CCGAT	-----CAGAA	-----GTAATA	-----TTCTGGCAGATAAGTAGTAGCTTCAATGAGG
Lm02	-----ATAAGTGA	AGGTGCTAAT	-CCAG	-----CAAAATGG	-----TGATTT	-----CCGTTTTGTAGATAAGAGGAGCTGGATATGTTGACTTTCC
Lm03	-----TTTACCGG	TGCTAAT	-CCAG	-----CAG	-----TATATT	-----CTGAAAGATAAGTCGSAATCCAAGTTTAGGAAACTCTAT
Lm04	-----TCACGGT	GCCAAAT	-CCAG	-----CAG	-----GTAAACA	-----CTGACAGATAAGGCACGCCGAATCAGGTAATTAAT
Lm05	-----GTGAAGG	TGCTAA	-TCTG	-----TTGCAGGAG	-----TATTAT	-----CTTCGACGATGAGAGGCAAGGTATAATAT
Lm06	-----TTGAAAAGG	TGCTAAT	-CCTG	-----CGAAGTG	-----TGA	-----TGCTGAGAGATAAGAGAGACTTAAAAAGTTTCAGTGTATTGT
Lm07	-----TTATGIGT	TAGGTGCTAAGT	-CATG	-----CAGAACAA	-----CTAA	-----TTGTTCTGAAAGATGAGAGGAAAGTTAGTCCATTTGAAAAAATGCT
Li01	-----GTTCTAT	GTCTAAT	-CCGA	T	-----CAGAA	-----TTCTGGCAGATAAGTAGTAGCTTTAATGAGG
Li02	-----GTAAAGTGA	AGGTGCTAAT	-CCAG	-----CAAAATGG	-----TGATTT	-----CCGTTTTGTAGATAAGAGGAGCTGGATATGTTGACTTTCCA
Li03	-----TTACCGG	TGCTAAT	-CCAG	-----CAG	-----TATATT	-----CTGAAAGATAAGTCGSAATCCAAGTTTAGGAAACTCTAT
Li04	-----TCACGGT	GCCAAAT	-CCAG	-----CAGT	-----ATC	-----ACTGACAGATAAGGCACGCCGAACAGGTAAATCACT
Li05	-----GTGAAGG	TGCTAA	-TCTG	-----TTGCAGGAG	-----TAATAT	-----CTCTGAAAGATGAGAGCAAAAGGTATAATATA
Li06	-----TTGAAAAGG	TGCTAAT	-CCTG	-----CGAAGTG	-----TGA	-----TGCTGAGAGATAAGAGAGACTTAAAAAGTTTCAGTGTATTGT
Li07	-----TTATGIGT	TAGGTGCTAAGT	-CATG	-----CAGAACAA	-----CGAT	-----TTGTTCTGAAAGATGAGAGGAAAGTTAGCCCATTTGAAAAAATGCT
Sa01	-----AGCACGG	TGCTAAAA	-CCAA	-----CGAG	-----TTA	-----CTCGAATGATAAGTATAAAGA
Sa02	-----GAAATGG	TGCCAAT	-CACA	-----TAAAGT	-----TTA	-----ACTTTGAAGATGAGAGAAACAATACTACTAT
Sa03	-----AAAAGAA	AGGTGCCAAA	-CCGT	-----TTGCAGAC	-----AAATAG	-----GTCTGAAAGATAGAGCGCAATGGACGTATTA
Sa04	-----ATGTG	GCCAAAT	-CCAG	-----TAACCG	-----TAA	-----TGGTTTGAAGATAAGCAGGTAAAGCACATGAAA
Sc01	-----CCGGCTAG	GGAAGGTGCCAAAT	-CCGT	-----CTCAGCGGG	-----AGATG	-----CGTCGTGAGGAAGATGAGGAGAAAAAGGGGCTCGGCTCCATGGCTGTGC

FIG.41-13

Ba15	-----TACAGGTGAATAGGTGCTAAAA-CCTG-TG-CGAGGCT-ACA-----GGTCTCGAACGATAAGAGCGAAGGCGAAAAAGCAGTATGCAAGTA
Ba16	-----GTTGAAATGGTGCCAAAT-CCTG-CAAGC-AAATG-----CTTIGACAGATGAGAGAGGGGATAATGTTGTTATATACGCAT
Ba17	-----ACGGAAITGTGCCAAAT-CCTG-CAGG-TAATAAAT-----CCTIGAGAGATAAGAAGAGCCCTTAGAGCGTGTTCCTCAAA--
Bc01	-----AATACCGTGCTAACT-CCAG-CAAGCCT-ATGAA-----AGGCTTGGAAAGATGAGAAGATGTGAACGAGTACATATAA-----
Bc02	-----ACGAAGGTGCCAAAT-CCTG-CAGGTG-AAGAAA-----CACCTGAAAGATAAGAGCGGTTCAATTAGTCAAGAAG-----
Bc03	-----AAGCAAGGTGCTAAAT-CCAG-CAAAATGG-AAT-----CCATTTTGAAGATAAGGTAAATATATAACCGAACAG-----
Bc04	-----GAGTGCTGTGCCAAAT-CCAG-CAAGC-ATAT-----GCTTGAAGATGAGAAGAGCGTTTCTTATAGATGTATAA-----
Bc05	-----TATAGGAAGGTGCTAAAT-CCG-CAGAGAACAC-GAT-----GTGTTTTTGGAAAGATAAGAGGATCTTGAACGTGAAAGAAAA-----
Bc06	-----TGAATACTGTGCCAAAT-CCAG-CAAG-GTAA-----CTTGAAGATAAAGAAAGAGCTCATTTTGACTGTATATGCAG
Bc07	-----AGTACTGTGCTAAGT-CCAG-CAAAAGT-ATGAA-----GCGTTTGGAAAGATGAGGGGAAATGGATTAAACATTCAA-----
Bc08	-----GCAGGTGCTAAT-CCAG-CAGAACCA-TATT-----TGTCTGGAGATAAAGACGAAAGATATATACGTAA-----
Bc09	-----GTAGACACGGTGCTAAT-CTCG-CAGC-ATTAC-----GCTGACAGATAAAGGAGCTGGTTGTAAAAAA-----
Bc10	-----GTTGAAACGGTGCTAATA-CCTG-CAAAAC-GAAT-----GTTTTGCATAATAAGAGAGGAGGATCGATTATGT-----
Bc11	-----GTTAATAAGGTGCTAAT-CCAG-CAAAAT-GTGAA-----GATTTCACAGATGAGAAGAGACTCTATTCAAAACCGAAA-----
Bc12	AAAA-----GGCACGGTGCTAAT-CCAG-CAGAAAGT-AAA-----ACTTCTGGCAGATAAAGAGGGGAGAGATAAACTTCAAA-----
Bc13	-----ACAAGTGAAATAGGTGCTAAAA-CCTG-TG-CGAGGCT-ACA-----GGTCTCGAACGATAAGAGCGAAGGGCAAAAGCAGTATGCAAGTA
Bc14	-----GTTGAAATGGTGCCAAAT-CCTG-CAAGC-AAAT-----GCTTIGACAGATGAGAGAGGGGATAATGTTGTTATATACGCAC
Bc15	-----ACGGAAITGTGCCAAAT-CCTG-CAGG-TAATAAAC-----CCTGACAGATAAAGAAAGAGCCCTTAGAGCGTGTTCCTCAAA--
Bc16	-----TGAATACTGTGCCACTT-CCTG-CAAGCT-TTAT-----AGCTTGAAGATAGAAAGAGGACTTCGTTTATATAGGGGTGCA
Bc17	-----TATAAGCTAAGGTGCTAAT-CCTG-CAAAACGA-GTTC-----TCGTTTTGGAAGATAAGAGAGGAATCTATTTTGTCTATTGG-----
Bc18	-----GGAAACACCGTGCTAAT-CCAG-CAAG-CAAGT-----CTTGAAGATAAGTGTATGGGCCCTTGTATTATAA-----

FIG.41-15

Cons	-----I----->	<-----I-----
	.yyyy.....	.rrrrr..tttty.....
Bs01	-----GTCCTCTT-----	-----AAGAGGACCTTTTATTCCTTTTTCCTGCTGATGTGAATAAAGGAGGCAGACAAI
Bs02	-----CCCTTCTTC-----	-----GAGAAGGGGTTTTTATTTTGAAAAGGAGGTGTCAGCTATAITGTCACAGCAGCTTGAAA
Bs03	-----GCCCTTCTC-----	-----GGGAAAGAGGCCTTTTGTGTGAGAAAACCTCTTAGCAGCCTGTATCCGGGGTGAAGAGA
Bs04	-----GCCCTCTTC-----	-----GAGAGGAGGCCTTTTACGGCCACATATAATTAATTACATAATTTGGAGTTATGATG
Bs05	-----CCTCTTAGAGCC-----	-----GCAGTTTGAAGAGGTTTTTGATATGGATGAAAATGAAGAGGCTCGGCATGAGTGAGTTATTA
Bs06	-----CTTCTTTCC-----	-----GGATTGAAAGTTTTTATTTTAAAGGTAAAGAGGCTATCTGTATATCAGCAGCGCGAAT
Bs07	TAACAGAGCGGCTATATGAACTCTTTCC-----	-----GGAAAGAGATTTTTTATGAAAATACGATGAAAAGGATGTTTTCAGCATGACGGTTT
Bs08	-----CCCTTTCC-----	-----GGAAAAGGTTTTTATTTTATTCATAAATATGCCAATTAACTTCTCTAATACTGTACA
Bs09	-----GCCCTTCTGC-----	-----GCAGAAGGCCTTTCTTTTGCAGAAAAACCGGAAGATTTCTTAGAATAGTGTAAAGGCAG
Bs10	-----GCCCTTCTCT-----	-----AAGGAAGAGCTTTTACATGCTTAATATTTTCAGAAAAGAGCGGAATAACAIGGCTCAACAA
Bs11	-----GCCCTTCTCT-----	-----AAGGAAGAGCTTTTATATTTGAATGGAAAGAGGAATGGACAACATGTCACAACAACA
Bh01	-----CAGGCTCTC-----	-----GAAGAGGTGTTTTTCTGTTTAAACCTTATCTGCGGAAAGATTACTTGTTATGTA
Bh02	-----CCCTTCC-----	-----GGAAAAGGTTTTTGTAGAGAGCCAAGTTTTTATAAAAATGAGGAGCGGCATACGA
Bh03	-----CACCTACTTCTCTCT-----	-----GAGAAGGTAGGTGTTTTTACAAATCAGAAAAGATCGAACTTTTTCAGATAGTTTAAAGAAAA
Bh04	-----CCCTTTCC-----	-----GGAAAAGGCTTCTCTCATTTTATCTTTTGAAGGTGCTGTTGGAAGATGAGTGCCGT
Bh05	-----CCCTTCTGC-----	-----GGGAAAGGTTTTTGTCTTATATGCAGTTTGATTCACGGAATTGCTACTTCTTACGA
Oi01	-----CCCTCTCTCT-----	-----AGAAGAGGGTTTTTGTGATTTTAGAATAGGAGGAGATTATTAAGAGCGGAGTTTACAAA
Oi02	-----CCCTCTCTCT-----	-----AGAAGGGGGTTTTTACTTTTCCCTATCTCTGTACAGAACTGTCATATGCTAGTTTCATA
Oi03	CTTCTTATCTTTATCATGTTTTT-----	-----AATAGAAGGGATGGATTTATATAIGACATACGGAATGGAAGATGAAACCGGA
Oi04	-----CCCTCTCTCT-----	-----GAAGAAGGTTTTTGTAGGGATGTTATGATGATTCAGTTGCGAAAAATATCGAGAAA
Oi05	-----CCCTTCTCAT-----	-----ATGAAGGAAAGGTTTTTGTGTTTTTATCTATAATTTTAGTACCGGTTTTTTAGTACGAGGT
Oi06	TA-----CGTCTTCTCT-----	-----ACAGAAAGGCTTTTATTTTGACGAATATGSGGAAACTATACGAAATGGTTGCTGGAGAG
Oi07	-----CTCTATCT-----	-----GGAAATAGAGTTTTTGTACATAGATGGCTCTATAATATTTGTGGGGTAAAGAAAAA
Oi10	-----CTCTTCTCTA-----	-----TATGAAAAGGTTTTTAAATTAAGATAGATAATGCGGGATGAAAATGAAGTATGGTTT
Oi08	-----CTCTTCTC-----	-----GGAAGAGTTTTTCTTGTGTGTCAGTGAGGGTTTGGAAAAAATAGTGAACAGTTTGA
Oi09	-----GTCTCTCTC-----	-----GAAGGGGGCTTTTTTAAATCTCTCTTATCTTTTAAAAATATAAATCAAGGAGGAA
Oi10	-----CTCTTCTCTA-----	-----TATGAAAAGGTTTTTAAATTAAGATAGATAATGCGGGATGAAAATGAAGTATGGTTT
Oi11	-----TCGGGAGGCTCTTA-----	-----TAAGGGCATCGGGATTTCTTATATTAATTTTAAAGGAGATTGGTAAAAATGAACAACAT

FIG.41-16

Oi12	GTACGAA	-----TCCCTCTTTCTCTG-----	-----TCCTT-----	-----CAAGAAAGAGGGA-----	TTTTTTTATTCGCTTGGGGTTGAGACATGATTGAATTTCAGAAATGTAACA
Oi13	TGTTA	-----TGCTCTCGAT-----	-----TTCAC-----	-----ATCGGGAGGCA-----	TTTTTTTAGTTCCGGAAAAATTCACAACATGAGAAAAGAGGAAGGATTTA
Ca01	-----	-----CTGCTCTTATTT-----	-----TTTAAT-----	-----GGATAAGAAGCAGT-----	TTTTTTTATTTATAGGAGGAGAAAGATTATGGGAGAAAATAGATTGTA
Ca02	-----	-----GCCGAGG-----	-----TTATTT-----	-----CCAAGGCT-----	TTTTTTTATTCCTATTTTTTAAGGGGCTAACTTATGAATCTTCACATA
Ca03	TAATAGA	-----TCCCTCTCTT-----	-----TTAA-----	-----AAGAAGAGGAT-----	TTTTTTGTTAATAATAGAACCACTTATTTATTTATTTGGTTTTTATCTTA
Ca04	-----	-----GAGCCAGAG-----	-----TTTAT-----	-----CTCTGGCT-----	TTATTTTAACTAATGGGAAAAGGTGAATGACATGATAGAAAATAA
Ca05	AATAA	-----TCCGTTTTTC-----	-----TTAT-----	-----GGAAATGGA-----	TTTTTTTATATATATAAATTTAAACTAGGACGGTGAAAAAAATATGCTTATA
Ca06	-----	-----TCCCTCTC-----	-----AACTAA-----	-----GAAGAGGATTA-----	TTTTTTATATATTTTTTAGGTTAGATATTGAAGTTAAATATAATAA
Ca07	-----	-----GTCTCTC-----	-----TTAT-----	-----GAGGAGAC-----	TTTTTTTATATTGTAGGAGGAAGTGGATATAATGAGAAAGTTATTAC
Cp01	-----	-----TCTCTCTTAAATCT-----	-----TTAA-----	-----AGSTTTGAGAAGAGAT-----	TTTTTTTATTAACAAAAATTTTTTAAAGGGCGGCATTTAAATAAAAGTTTGT
Cp02	-----	-----CTCTATC-----	-----CTAG-----	-----GATAGAGTTTTTT-----	TTTTTTTAGGATAAAGGATAGATTTTATAATGGATTAGGAGGA
Lm01	-----	-----TGCTTCGATCTG-----	-----ACCAAAAA-----	-----CAGAGGAAGCGT-----	TTTTTTTAGCGCTTAAGAGGGGAGTTTTTGTAGATGAAGAAAATTTT
Lm02	-----	-----ACTCTCTATT-----	-----CTAA-----	-----AATAGAGAAG-----	TTTTTTTATGCTTTCATGAATAAATCTGGATAATCACACAACATACTAGG
Lm03	-----	-----CCCTCTCGCG-----	-----CTTATATA-----	-----CTGCTAGGGAGG-----	TTTTTTTGATGGAAATTAAGTATAAATACATATCAAGAGGAGTGGATTTTA
Lm04	-----	-----CTTCCCTTAAAG-----	-----CTGT-----	-----CTTTAAGGAAAG-----	TTTTTTTATACATAAAATATAAGAAATGAGCGGAAGAAAATGAACCAAG
Lm05	-----	-----AGCCTTCTCTATTCGTGGCGTTTT-----	-----GTGCAAAATAGAGAGGCT-----	TTTTTTTATATGAGACGTTATTTGGAGAGAAATGAAGAGGAAAAATAAAATTTGG	
Lm06	GTATCGAAACTTCCAAA	-----CCCTCTCTAG-----	-----TTCT-----	-----CTAGGGAGG-----	TTTTTTTATTTGGCAAAAAATCGAGAGGATAAGGTGATAGGTAIGGTAAGGCG
Lm07	-----	-----GCCTTCTGCT-----	-----CATC-----	-----AGCAAAAGGCT-----	TTTTTTTGATATCAGAAATGTAGAAAAGGTGATAGAGATGATTACGTTACA
Li01	-----	-----CGCTTCGATCTG-----	-----ACCAAAAA-----	-----CAGAGGAAGGTT-----	TTTTTTAGCGCTTAAGAGGGGAGTTTTTGTAGATGAAGAAAATTTTA
Li02	-----	-----CTTCTCTATT-----	-----CTA-----	-----AATAGAGAAG-----	TTTTTTTATGCTTTCATGAATAAATCTGGATAAATAATCAACATACTAGG
Li03	-----	-----CCCTCTCGGG-----	-----CTTATATA-----	-----CTGCTAGGGAGG-----	TTTTTTTGATGGAAATTAAGTATAAATACATATTAAGAGGAGTGGATTTTA
Li04	-----	-----CTTCCCTTAAAG-----	-----CTGT-----	-----CTTTGGGGAAAG-----	TTTTTTTGATACATAAAATTAAGAAATGAGCGGAAGAAAATGAATCAAG
Li05	-----	-----GCCCTTCTCTATTCGTGGCG-----	-----TTT-----	-----CGTGCAAAATAGAGAGGCT-----	TTTTTTTATATGAGACGTTATTTGGAGAGAACTAAAGGAGGAAAAATAAAATTTGG
Li06	GTATCGAAACTTCCAAA	-----CCCTCTCTAG-----	-----TTCT-----	-----CTAGGGAGG-----	TTTTTTTATTTGGCAAAAAATGAGAGGATAAGGTGATAGGTAIGGTAAGGCG
Li07	-----	-----GCCTTCTGCT-----	-----CATT-----	-----AGCAAGAGGCT-----	TTTTTTTGATATCAGAAATGTAGAAAAGGTGATAGAGATGATTACGTTACAG
Sa01	-----	-----CTTCTTACTTT-----	-----TCAAT-----	-----AGGGTGAGAGG-----	TTTTTTTIGTTTAGGAGGAAAAGCAATGACAAATTCACAGTAGATACTT
Sa02	-----	-----TGTCTTCTCAATTTT-----	-----TCTATC-----	-----GATATTGAGAAAGCA-----	TTTTTTTATTTAAGCAACACAGGGAGGAATCAACGTGATTGAATTA
Sa03	-----	-----GGCTTCTCTCTAT-----	-----ATTA-----	-----ATAGTTAGAAGGCT-----	TTTTTTTATTTAGTCCACAGAGAGAGAAATTTTCGTAATATAAATTTAAAGGA
Sa04	-----	-----ACCTCTTCTTCA-----	-----TCGTT-----	-----TGTGAGAAAGAGG-----	TTTTTTTAAATTGGAAAGCAGGTAAAGGATGGAAGTACATAAAAGAGCA
Sc01	AGACTGCCGAACCTCCAGAAC	-----	-----	-----CCACCGAGCGCGCGCTCGACCTCGGCCCGCCCGCCCGCTGAGCTGCCGGG	-----

FIG.41-17

Cons	-----T-----> -----T-----<-----T----- .yyyyy.....rrrrr.tttty.....
Ct01	CTTGATGCTTCGGCACATACCTCTGACCCGACGGCAGCTAGGATCGAGGCTTCAACCTTGTTACCATTTGCCATGAGTGAGGATAACACCTTCGGTTCGAGACCTTCGAGGTTCCAC
Tt01	-----CCTCTTCT-----TTT-----AGAAGGGTTTATTTTGCTCTTAAGGAGGAAGAAGATGCGTAGACTCTTTACTTCTG
Tt02	-----GTCTCTTC-----TTTTAGC-----GAAGGGACCTTTTATTTTAAAAAGGAGGGGCAATTAAATGTTGAAAAATGAAAAGCT
Tt03	-----TTACTAGGCCCTCTTC-----TCATT-----GAAGAGGCCCTAAGAAATTTCTGGAGGTGCAAAATGAGGTAAGAATGGGTGATGGGACTTGGA
Ft01	-----CTCTAICT-----GGAATT-----GGATAGAGTTTTTATTTAATATTTTGTAAATTTTAAAGAGGGAAAAATGAAAAA
Ft02	-----TCCATACT-----CTATAA-----GGTATGGATTTTTTAATTAAAGTAAGAAATTTATATAGAAAGTAGGGATATAAATGATTAA
Dt01	-----TGGCGTCCCTTCCAGACTTCTTTTGGTCCAGGAAGGGGAGCCCGTTTTGGCCGACCTCTCGCTCTCCCAACGGAGGCCCGCCCGTGACCTT
Dt02	-----CATCACCCAGAGGGTCGGCTTCC-----GCCAATCCGTCCATCAACCATCAACCGTCCACCATCACCGAGGCCGCCCGC
Xa01	-----GAGCTCC-----GCGAAGCTCGATGGCC-----GATCCACCTCGATACCGCATGAGCCCTGTAATCTGATCGCGTCTTA
Xc01	-----GAGCTCCCGCGAAGCTCGATGGCC-----GATCCACCCCGGATATCGCATGAGCCCTGTAACACAGCATCGCCACTCA
Se01	-----GTGCCTTTACATC-----ATTT-----GAGTAAGGCACTTTTTTAGTTGAAGGAGGTAGGAACATATTATGACGAATTACACGGTTAATA
Se02	-----TATCTATA-----
Gs01	-----GGCCCTTCCCG-----TTTCC-----CGGAGGGGGCTTTTCATTTTGGCCGCGCGCGACGCGCCGTGGGAATCATGTCTCGTGG
Gs02	-----TCTCTTCCG-----CACCC-----CGGAAGGGGATTTTTCATTGTGAGGAACCATGAACATCGCGACGCGAGGCAGCACAGATC
Ba01	-----GCACCTCTC-----TTATTTT-----GAGAGGTGCTTTTATTTTGGAAACATATAGAAGGGGAACTATAGATGAAAAAGTATT
Ba02	-----GCCTTGATCTTA-----TTTTT-----TAGGATCAAGGCTTTTGTATCTAAAAGAAAAAGGGAGTAATGGAAGAAAGTACGTTTCTATA
Ba03	-----TCCCTCTTCTC-----AATAC-----GAAAAGAGGGATTTTTTATTTTTCATTTCCCTCATCATCATCCAACCTTAATTTATTTAGGAG
Ba04	-----GTGCTCTCTCTTATC-----TTTATGGTT-----GATAAGAAAGGAGACACTTTTATTTTACCTGAGAGCTCTACTTCAAGTTTTTACAGCATATAGGAG
Ba05	-----CTCATCTTTC-----TTGATCAT-----GAAAGGTGAGTTTTTATATTTTCAAAACATATATGGAGGTATTTAAAAATGAAAGTAAIT
Ba06	-----TCTTTTC-----GAAATG-----GAAAGATTTTTTTTATGAATAAAAAGGGGGCTGTTCCGCTGAGCGTACGGGAACAT
Ba07	-----GACCTCTTCT-----CGTT-----GGAAGAGGTCCTTTGTTATTCATTAGAAAAAGGTGAAACTAGGAGAGATGGTACTTTTG
Ba08	-----TGACCTCTT-----ATGT-----AAGAGGTCATTTTTTGTTGATAGAAAGGGAGTGTGATGCTAATTCATTTTCAAAATA
Ba09	-----GCCCTCTTCTA-----TCTTT-----TAGAAGAGGCTTTTTTACGTGAAAAATAAAGGAGGAAGAAAAATGGGAGGCACAGGAGTAG
Ba10	-----CTTCTTC-----TTATC-----GGAGAGGTTTTTTTATTCGAAAAAACCGATTACGAAAAAATTTATATTAAAGAAAAA
Ba11	-----CCCTCTTCT-----TAGT-----GGAAGAGGTTTTTCTACGTGAGAAAAACCTCTGAATGAAAAAGGGGGAGAGACGATG
Ba12	-----CCCTCTC-----CTTAGCT-----GAGAGGTTTTTTTATTTAACTAGGAGGTATTAACAAATGAGCGGAATTTATAGCGACGT
Ba13	-----GCCTTCT-----TCTT-----GAAGGCTTTTTTATTTTATTTCACTACTGTTCAATTTAAAAAGGAGGAATTTT
Ba14	-----CCCCCTTCA-----AAG-----TGAAGAGGGGGTTTTTATATGATAGAAATGAGGAGATTTTGTGAAATTAAGTATTTATTTG

FIG. 41-18

Ba15	GCAAAATTAAA	-----	CGTTCCTCT	-----	ATATAA	-----	AGTAGGAAGGTTTTCTGTATGCTTGTGTGGGAGAAATAAATGTATGTGCGCAATCTGTGGCA
Ba16	ATAAA	-----	CCTTCCTGCTT	-----	CTCTA	-----	AAGCGGAAGGTTTTTGTGTTGAAATGTGGAGGACATTCAAATAATAAAAGTAATGAGA
Ba17	-----	-----	CTGCTCCTTCCTTG	-----	TTTT	-----	CAGGAAGGGGCGAGTTTTTATTTGTATATAAAGAAAGGAGAATGAGAAATGGGAGAAATCATGGG
Bc01	-----	-----	GTGCTCTCCTTCCTTAATC	-----	TTTATGGTT	-----	GATAAGAAGGAGAGGACATTTTATTTACCTCGAGAGCTCTGCTTCAAGTTTTTACAGGCATATAGGAG
Bc02	-----	-----	GCTACTCTTAAT	-----	TTGG	-----	ATAAGAGTAGCTTTTTTATGGCTAAAGTTAAAGGGGAAATAGGTAGTGGAGTATGGTTTT
Bc03	-----	-----	TCTTTTC	-----	GAATG	-----	GGAAAGAATTTTTTATGAATAAAAGGGGGCTGTCGCGTGAGCGTAGCGGAACAT
Bc04	-----	-----	GACCTCTCT	-----	CGAT	-----	GGAAAGAGGCTTTTTGTATTCATTAGAAAAAGGTTGAAACTAGGGAGAGATGGTACTTTGA
Bc05	-----	-----	TGACCTCTT	-----	ATGT	-----	AAGAGGTCAATTTTGTGTATAGAAAGGAGTGTGATGCATAATTCATTTTCAAAATA
Bc06	AA	-----	GGCTCTTCTTA	-----	TCITT	-----	TAGAAAGAGGCCTTTTTATGTGAAAAATAGGGGGGAAAGAAAAATGGAGCGACAGGAGTAA
Bc07	-----	-----	CTCTCTTAAT	-----	ATGT	-----	GTAAGAAGAGTTTTTATTTAGAGAGGGGGATAGAGTGAAGTTTGATGTAACGTATTTTT
Bc08	-----	-----	CTCTCTC	-----	TTATC	-----	GGAGAGGTTTTTATTTGCAAAAAAACCGATTACGAAAAATTTATATTAGAAGAAAAAGG
Bc09	-----	-----	CCCTCTC	-----	CTTAGCT	-----	GAGAGGTTTTTATTTAACTAGGAGGTATAACAATGAGCGGAATTTATAGCGACAT
Bc10	-----	-----	CCGCTCTCTCA	-----	AAG	-----	TGAAGAGGGGGTTTTTATATATGATAGAAATGAGGGAGATTTGTGAAATTTACTAGATTTATTA
Bc11	-----	-----	GGCTCTCT	-----	TCIT	-----	AGAAGGCTTTTTTATTTTATTTTCAACTAATGTTCAATTTTAAAGAGGGAATTTTC
Bc12	-----	-----	CCCTCTCT	-----	TAGT	-----	GGAAAGAGGTTTTTCTACGTCAGAAAAACCTCTGAATATAAAAAAGGGGGAGAGACGAT
Bc13	GCAAAATTAAA	-----	CGTTTCCCT	-----	CTCTATTATGT	-----	AGGAAAGGTTTTTCTGATGCTTGTGTGGGAGAAATAAATGTATGTGCGCAATCTGTGGCA
Bc14	ATAAA	-----	CCTTCTGCTT	-----	CTCTA	-----	AGGCAGAAAGGTTTTTGTGTTGATGTGGAGGACATTCAAATAATAAAAGTAGTGATA
Bc15	-----	-----	CTGCTCCTTCCTTG	-----	TTTT	-----	CAGGAAAGGGGCGAGTTTTTATTTGTATATAAAGAAAGGAGAAATAAGAGATGGGAGAAATCATGGG
Bc16	TAACTGTAGCTAAAAA	-----	TCCCTCTCTC	-----	TCAATAT	-----	GAAAGAGGGAATTTTTATTTTCAATTTCCCTCATCATCCAACTTAAATTTATTAGGAG
Bc17	-----	-----	GCACCTCTC	-----	TTATTTTT	-----	GAGAGGTGCTTTTTTATTTTGGAACGTATATTTAGGGGGGAATTTAGATGAAGAAAGTAT
Bc18	-----	-----	GGCTTGATCTTA	-----	TTTTT	-----	TAGATCAAGGCCTTTTGTATTTCTAAAAAGAGAAAAAGGGAGTAATGGAAAAAGTAGCTTCATA

FIG.41-19

Cons
Bs01	GGGACATTTAGAAAGATTTGCAAGACAGGTGTTAATCGGTGACGGCGCCATGGGACGGCTCCTCTACTCTATGGCATTGACAGGTGTTTGAGGAGCTCAATATTTCAAAGCCGGAGGA
Bs02	CGAAATTAGCTCAAAATTTGGGAACCGTAGCGATGAAGTACAGGGAACAGTGAAGTCTCTATCTATTTATCAACAGCATACCGCCACAGAGGATCGGAGAACTCTACCGGATTTGATTATG
Bs03	GTGTTTACATAATAAGGAGGAGAAACAATGACACCATCAAAACATCGAATTTAGGATTTCCGAGATCGACCTGAACCGGGAATGGAAAAAGCACCTTGAAGCGTATTTGGAAAAAGGCAG
Bs04	GGAGTCACAAAACACCTTTATACGAAGCTTAAATGAAGCTCCGCTGTGGCGTTGAGCTATTTCCAGCAAAAGCACCGCTGACATGCCAGGAGATCGGAGAGCGGC
Bs05	GGGACATATCTCTGACCGAACCGGAGCGGATACAGAGAAGAACAAATCGCAACAGGATTGACAGTAGGCTCTGGACTGATCTGCCCTTGTAAACAGGAGCAAAATGCAA
Bs06	CACATTTACATGGGAAAAGACACCGGCAGAAAGCTACTGTTTGTGTTCCGAAGGAGGAAAGAAATGTTAAGTATGATAATTTGGGAAGAACCAACGATTACATTTCCGGGAAGA
Bs07	TGGTTACAGCACCGTACAAAGAAAGGACGAAAGAGCTTGAACCTTGTGGCTCAGTTGCTTATCAATCTTGAAGGAAACAAGGTAGGGCATATCGGGAGGATGAACCTCATTCAGC
Bs08	TTGTATAGAGGAGCGAGTTCGTATCATATATACAGGCTTTTCGGGAGGCCCTTGTGAGGAGGAGCAAAATCATGAGTAAAAATCGTCGTTTATTTACATCAGAACTCTGTACGGAG
Bs09	GTGATTGCTTTTGATCAATCTTCAGGATGTTTCAAAGTTTACAAGTCGAACATGGAGATGTCAATGCTGTCCAAAAGCTCGCTTCCATTAAAAAGGTGAGATTTTGGAAATTATA
Bs10	ACGAATGTTGAGGACAAAAACAGAAAAACAGCAACACCTTTCGGCGCGATCATGTCCGAGCTTGGCTCGGTTCCGGTAAAGGAAGCCGGCAAAAAAGCGCGCTGGT
Bs11	ACACCGCAGAAACAAAATCACCTTCAAAGAAAAAACCGCGTTTCGGCGGATCAAGTCGGAAGCTGCTAAGATCTGAGCCGCTCAAAAAAGCGCGCTGCAAAAAGCGCGCGCGAA
Bh01	CGAAAAACAGCAAGACAAAAAAGAACAACTTGGAAATGAGGAGGGTGTACATGAAAAAAATTTAGCTAATCCACGAAAAACGATGAATGGACGGTTCACTTATTTAAACGACTTGAGGA
Bh02	AAGGGGAAATTAATCAGATGATTAAGTTGGTGATCGGATTTGGCACCGTTGGGCAAGGTGTGTCGAGAGTCTAGTTCAATTTGGAGCGAGGATTAAGSAAAGAAAGTTACTCTCGAAT
Bh03	TGAAGGCTTCGCAACTTGGCAGCAGCTGATTTTCCAAATAGATGGATAGGAGGACCACTGAATCGTAAAGAAATAGAAACAGCTTAGTACAAATCGGAAATCGAATCGATGATC
Bh04	ATCATGTTTTCGGCAGCCTGCCGTTGGTAAGGGTGCTTAAGGAGGATATTCGTAATGGCAGATACAAGAGTCTGCTGCTTATTTACATCAGAGTCTGTACAGAAGACATCCTGA
Bh05	TAATGATTTGCGTGCTCTTGAGACGAAATTTGGGAGAGTGAGAGTTTTCGCTCGTACTGACTTTTCGTTAAATTTGGTAACGGTAGACGAACTGATATATTTTGAAGAGGGCTT
O101	GAGGTTTGCAAGAGGACGGTAAATAGCAGGAGAGGGGTATTTTATTTGAATTAGAGAGGAGGGGTACTTACAGGCAAGTTCGTTTGTACCAAGTAGCCCTTGAAAAATCCGGATGGGT
O102	GAGCAAGACCCCTACTCTATAAGACTAGCCCAATCTAAAGGAGAAAGAGGAAATTAACATGACAAAAACAGTTATTAAGCACCATTTCGGCGAGACCATGTAGGTAGCTTACTACGAC
O103	ACAAGAAAGAAATGATCTAAATTGAGAAATTAATTGCATCTAATCAATTTAAAAAGGGAACAACATCTATATGAACCTGACACAGCAGAGTTGGAAATAGCAATACTTTAAATTACAATA
O104	CACATGAATCTAAAAAGAGAGAGTATAGGGGTAGATCAAGTTTCCCTTGATATCAAAAGGGAGAAATATATGGCATCGTTGGATATAGCGGTGCAGGTAAAGTACGCTTTTAGGT
O105	TCCTTTATTGGCCTTTTGAATAGGATAGAGTTATAAGAGATCGGTACCAACATATATCAAGGAGAGTTTAGCCTTAGGCTGCAAAATCGACGTTTATTTACTTCAGAGTCAGTAACCT
O106	TAAGAGGAGGAATAAAGATTGATATCCATCGAAGGGTTAAGTAAAGTATTTTCATTAAATAAAAAGACATCAAGCTCATTGACCCCTCAATATTTGAAAATGGCGATATTTAT
O107	TAAAAACACGCAATCTCTATTTTGTATCATTTTAAACCCTAAACCAAAAAAGGAGATGGTGCAATTTGAATTTCTAACATAACATTTACCTGGGTTGGAAGAAGGAAATATA
O110	CTGGTTGCCGATTTTGGAGGGTGGTTGGGTAATGTAGAGATGAACAGATGCCCTACTTTTGAATATGCAAAACAGGTAAATTCAGCAGCGGAGAAATGGGGATATGATACGACTTT
O108	CTTCAAAATATGAGTAAACCAATCAGTAACTAAGTAGGGGATCGAACTGTCAAGTGATCGTAGTTTATAAAAATCTAAATTAAGAGGAGAGCGGTGTATTTATGCCAACTATAAAAC
O109	ACAGGATGCTAAATTTCAATCTTTGCAAGCAGAAACAATCTTACTTCAGGAGCAGGAACCCAGACCCCACTCAACTGGTTCAGGTGAGTTCCAAATTTATCAAACTACGCTCTATGTT
O110	CTGGTTGCCGATTTTGGAGGGTGGTTGGGTAATGTAGAGATGAACAGATGCCCTACTTTTGAATATGCAAAACAGGTAAATTCAGCAGCGGAGAAATGGGGATATGATACGACTTT
O111	TGTGACATTTGTCGGCAGCCCTCCGAACTATCTAGATCTGAAAAAGTACTACATTTATTTAGGGAAATCAATTAAGTGAACAGAAATTTCTATGTGACCCCATATTTCTGTTAAAGATGTACC

FIG.41-20

0i12 AAGACATTCACACTAGGAAAAAGTAGAAGCTGTTAAAGAAGTATCTCTAACGATCGAAAAAGGAGATATTTATGGAATTTATGGGTTACGGGTGCAGGAAAAAGTACCTTGCTT
0i13 IGTCCACATCGATTGTAAAGAGAGCTCCGGGTCAATTATCGGATTGGCGGGATGCTCTGGAGGAAATTCCTGTACTGCTGAAGAAGTGTAGTTAATGTTATACAAGTTATCGCAGGGA
Ca01 GAAATTTTGACACAAAAGCAGTTCATGGGGAGAGTGGTTTGAGAGCAGAACTGGGGCAATAGCTACCAATATACCAAGTCTTACCTTTAGACATGAAGCTTAATTAAGGSAACGTG
Ca02 AAGAAATTTGTTAAATAACAAAATTTAGTTTATAGTGGTGTATGGGAACATGTTCAATCCCTTAATCTAGTAGAAGCGGACCTTAAAGGTTCTTATCTTGACATGTCATTCCAAT
Ca03 TTAAGAGTGGTATAGGACATAATTTTAAAGAGAGAGAAATACCTCCAAATATTTCTCCCTCAATCCATAAGCTTATAGATTTACCCAATCTATCCTTAAATATATTTTACTA
Ca04 AAATGTTTCTAAATATTTTCAGGAAATAAGTCTTAAAGATGTTGATCTGAAGATTAAAGCGGAGAAATATTTGGAATTTGTTGATAGTGGAGCTGGAAGTCAACATTACTTAG
Ca05 AAAATACCTGATAATCTCCAGCAGCAAAAACCTTAAATGAAGAAAATATATTTTATGGATGAGGATAGAGCCTATCATCAAGATAAAGACCTCTTAATATTTAGTTAACTTT
Ca06 AAGGGGATTTTAAAAATGAGTGAAGAAAGAAAATTTGGTTTGAACATACAGGTTCAATGACGACAAAGTTGCTGATCCAACTACAGGATCAAGAGCTGTAACCTATTTATCAAAACA
Ca07 ATCTGAATCAGTAACAGAAGGGCATCCAGATAAAATCTGCGATCAAAATACAGAGCTATTTAGATGCCATATTTGGAAGAAAGATCCAAATGGAAGAGTGTCTTGGAAGACTACAGTGAC
Cp01 TAATTAAGCTTTAAAGATATTTTGAATCGTGGGAAGATAAAATTAAGTTATTTGTTTAAATAAACAGGTTGGAATAAATAAAATGAAGGGGTGAATTAGCTATCTTATATGATA
Cp02 GAGAAAATGAAAAAAGGAAAGTTTCAGCATTAATACATTAATAATTTTGTATCGATTTATTTGGSACTTCATTAGTAATGAAGAATTTCTACTCTGTATCTGTTTAGTTCAGGA
Lm01 TATTAGTAGCGGTTATCTCGGTTTTCGCTTTGGTTTAAACGGCTTCGGAGGTTTCGGCGTAGTTTCAGACAAAGCAACCGTTTCAGSCAAAGCGAAAGACGGCGGCTCTCTTATTATCG
Lm02 GAGGAAAAAGATGAAAAAATTAACAAAAGGGTTAGGAAATTTTACTTGATCAAGCTTTGTTTAAAGATTAGCAGATGTTGGAGGAGGAGTGAAGTAAAGCTTAAGCACAGAAAAA
Lm03 TGAGTAATGAGTATAAATTCGAAACAAATCAAGTACAGCGCGGACACACCCGACGGAGATACACATTTAGAGCGGTACTTATTTCAACGACGTCATACACATTTGATAGCCCGG
Lm04 TAGCTCCATTTATGAGATCATGTGGGAAGTATTTAGCGACAAAGGGAATTAAGAGCCAGAGAGAAATCCAAAGTGGCGAAATACAGCTTAGAGTTGCGCAAAATCGAAAAATA
Lm05 CTAAGAACCGTCATCTATTACATCAGAAATCGGTTCTGTATGACATCCAGATAAAATTCGAGATCAAAATCTGATGCAATTTAGATGCAATTTTCAAAAGATCCGACGGCGGTG
Lm06 GATTAGTTCAAACTTGGGTTATCGAGACTTGGGGAGAAACGTGAATGGAACGTGGTTAGAAAAATTCGGAATGGTGGATTTTCGGAAGAGGAATTTGTTGGCTGAAACGAAGGCTCT
Lm07 AAACGTTGTTAAAGAATACAGTCCAGAAACAAACAAAGTTCTCGCAGTCGATCAATGTCGATTAGAAAATGAACAAGGCGGAGATTTTCGGAGTTGTTAGGTTATTCGGAGCTGGTAAAG
Li01 TTAGTAGCGGTTATCTCGGTTTTCGCTTGGTTTAAAGGCTTGGGAGGCTCTGGCGCTAGTTTCAGACAAAGCAACCGGTTTCAGGCAAGCGAAAGAGCGGCGCTCTCTAAATTTATCGGT
Li02 GAGGAAAAAAGATGAGAAAATTAACAAAAGGTTAGGAATTTTACTTGATCAAGCTTTTCTAGGTTAGCAGCATGTTGGAGGCGGAAGTGAAGCTTAAGCTTAAGCACAAGAA
Li03 TGAGTAATGAGTATAAATTCGAAACAAATTCAGTACAGCGCGGACATACACCGGACGGAGATAGCATTTCTAGAGCGGTACCAATTTATCAACAACATCGTATACATTTGATAGCCCGAG
Li04 TGGCACCATTTTATGAGATCATGTTGGAAGTATTTACGGACAAGGCAATTAAGAGGACCGGAGAAATCCAAAGTGGCGAAATTCAACTCAAGAAATACGTGAATTTGAATAATG
Li05 CTAAAAACCGTCATCTATTACATCGGAATCGGTTTCTGATGACATCCAGATAAAATTTGAGATCAAAATCTGATGCAATTTTGAATGCAATTTTCAAAAGATCCGACCGCACGTG
Li06 GATTAGTTCAAACTTGGGGTATCCGAGACTTGGGGAGAAACGTGAATGGAACGTGGCTAGAAAAGTTTGGAAATGGTGGATTTTCAGAGAGGAATTTATGCGGGAACCAAAAGCTCT
Li07 AACGTCGTAAGAATATACGTCAGAAAATAACAAAGTTCTCGAGTCGACCATGTCGATTAGAAAATGAACAAGGTGAGATTTTCGGAGTAGTTGGTTATTCAGGGGCTGGTAAAGT
Sa01 TAAATCTAGGGAATTTATACAGAAATCTGGGAAGTCATAGATAACTTCGCTTGAGATATAGCATGTTGGTTATCATGGACAACCAATAGTTGTAGTTGTGATGCTAATCTAAGTGGCA
Sa02 AGAAGTTGTTAAAGAATATCGACTAAAAATAAAGAAGTCTCTGTAGATCAGGTTAAATTTATCGATTGAGAGGAGTGAATTTATGGCGTCAATTTGGTTTTCTGAGCAGGAAAAAG
Sa03 GCAAACTATGTTAAATAACAAACGATTATTACTTCAGAGTCGTTACAGAGGACACCCAGATAAAATCGCTGACCAAGTGTGAGTGAATTTAGATGCTAATTTTAAAGAGGACCC
Sa04 ATGCTGGGCAATATTCCTTGTATTTATTTGGGGTGTGTTTATGGGGTAGGTTATTCACAGGTGATTTTACTTCAATGCCATTAAATGTTGCAATACGATAACGTAATTTGTGG
Sc01 AGTGGGCGCACAGGGTTTCGGCTCGGACCGGCTCTCGGCTCGGAAGAGTGTTCGGGCGGCTCGAGATCGGCTACGACTCTCGGACTACGACCGGAGAGCTGGGCAAGCGGATGGAAG

FIG.41-21

Cons
Ct01	GCCTGGGACGAGCCGTGATCGGTGACGGGATGCGCGCGGTGCCCATTTACAGACCACTCTCTACGTGTTGAGAACGCGGAGCAGGGGCTGACCTGTTGCGGCTTGGCAAGGCGGGC
Tt01	AGTCAGTCACTGAAGGGCATCTGTGACAGATCTGTGACAGATTCAGATGCCATTTGGATGAAATTTTAAAAAAGAACCTTACGCCCGGTGGCATGTGAGACAGCTGTAACTACCG
Tt02	GTGTAATAACTTAAGAAAGAAATTTGTAATAACTGTGAAATTTCTCCCCCAAGGGATAGATGTAATACTAACTATCGAGAGAGCTCGAAACTTAAAGGTGTGGCAGATGCTCT
Tt03	ACTGTGGGACAGAGTATTTAAATAGTTAATCTAGAGGAGATATACAGGAGAGTACGGGATTTATCCGGAGATAAGAAAGTGTGTGAAGGATTTGCACAAAAAGAGAAAA
Fn01	GTTTACATACTTTACATCAGAAATTTGTTTCCACGAGCATCCAGATAAAATTTCCAGATCAAAATATCAGATGCAATTTAGATGCTTGTTTAAAGATGACCCCTAAATCAAGAGTTGCCTG
Fn02	CACCTGAAAATGTAAATAAAATTTATTCCAATAACTTGCATGCTGTAAAAGATGTTAATTTAAAAGTTAATGAAGSAGATATCTTTGGAAATTAAGTTTAAAGTGGTGTGAAAAATCTT
Dr01	ACCGTCTCCCCCGAGCTTGACCTTCGAAGGCGTCAGCAAAACCTACCCGGCCAGCGCGCGGCTGAGCGATTTGACCTCACCGTTGCGCGGCGGAGCCGACCGGCATCAT
Dr02	CAGCGATCCTGATTTCTGACGGCGCTTGGGTACCGAGCTTCAGCGAGCAACCTCACCGAAGCGGACTTCGCTGGGAGCAAGCCGACCCACCGGATGTACCGGGGCAACTTCGAC
Xa01	CCAAGATTTGTTGACACCCCGCAGCAGCAGCGGATCACTGCCGTGGCGGGGAACTTGTCAATGCCCTGCCGATGCCCATGCCGATGCCGAGCTGGCGCTGGCTATG
Xc01	CCACGCTGACACCTACCGCCCGCTGATAGCGAGCCCGCTGCCGTGGCGGGGAGCTGCTCAATCTACCGATGGCCAGCGCGGCCAACCGGAGCTGGCGCTGGCTAGC
Se01	CATTAGAACTAGGTGAGTTTAAAACTGAATCTGGTGAACGATTTGATCATTTAGCTTACGTTATGAACATGTAGGACTTCTTGGTCAACCCCTTGTGTTGTTGCCATGCACCTACTG
Se02	-----
Gs01	CATGTCGAAGAACAAATCCGTCACTTCGAAGGGATCTCAGCTTGAAGCGCGCGGATCTGCGGCCCATCACCTGGCTACGAGACCTACGCGCGGCTGAACGCGGACCGGTCCAA
Gs02	GGTCTCGACTGGGATACCGGACCGGGCGGTACCGGTACCCATCTACGAGCGCAACCTTCGGGCATTCGGGATTTGGCCAGAGCAGCGGTACGATTAATCCCGCTCCGGCAACCCC
Ba01	ATTAAACATTGTAAGCGGAGCGGTACTATTATTAGCGCATGTAGCGTGGTTTCGGATAAGAGTAAGAGCTTAGATGAGAAAGATTTACTGTGCTGTAAACAGCGCGGCGGCATGA
Ba02	AAACAAAGTAAATTCATGTGTTTAGGGGTTATGGAAGTGTATGTAATTAANAATATCGGTTATGGTTCACACTATGGGTTATTACGACAGTGACATTTCTAATTTATGCAATTAT
Ba03	GAAATCAAAATGAAAAGAAAGTTGTACCCGTTATGATCAGTTGTAGGAGTAAAGTATTTTAACTGGTTGCGGTAGTTATAAAAACGAAGCAAGCGGAGCAAAATGCAAAAGACGAG
Ba04	GGGAAAAATGATTTCTTTAATGTAAGTAAAGTATATGAATCAGGTGGGCAATCTGTTCACTCGGTTGGAGGATTAAGCTTATCAGTTGAGAAAGGCGAAATTTTGGCATTTATCG
Ba05	GACCTATCACAACATTCGAAAAATAATGCTCAATTTCCCTGGAACCAAAATCAATTTAGAGCCATACAAGCGTTGAAGAAACAGGTTATCAAGTTACAGATTTCCATTCTGTC
Ba06	TTTGAGGAAGTCTGAGAGAAATTCAGCGGATGCTTGCATATGAATAATGTTTCAATTTGTTCAAGATGGAAGAGTCACTCACTAGAGAAAGTGAAAGAGTAAAGTAAAGTAA
Ba07	AAAGAAACGAGAGGAAATGTTTGGCTTTATTACCACTTGGGATATTTTGGCGTATTTATAGGTTCTGGAATTTATACAGGTGATTTCTATAAATTCGCGATCTTGTAGCAATTTCA
Ba08	AAATAGAGTAAATAAAGTTGACTATTAAAGAGGGGAAATTAATATGAACAGATTTATCAACAAAATAGTAGTAGCAATCGGAATTTGGATCAGCATTTATACGGGATTTAGGACTTTGGG
Ba09	CGTCACAAAGAAAAACAAATGAAGAGATATGAAAGAAATAAGGAAAAAGTACATAGAAAACAGTCATGATTTATCGGAAATCCGGAGATTTGGTAATCAAGAAATTTACGCATCTAGAA
Ba10	GGGGTTCGAAGTACTGTGACACTCGAAAAATACGTAATAACTGGGTAGTACAGTTATGAAATATATGATAGAGCAAGATAAGCCAAATATCATTTAGATATTTCAAGAACATATCGTTTC
Ba11	GGATATTATTCATTAAACAGAGTAACCGCTGTACAATATCGGAAAGAACATGGTTATTTTGAAGAAAGCAATGTAGTTTGTATGAAATTTGGAGATGGAATTTAAATATGTGTTTC
Ba12	ATTTAATCCATGATGATTCACATAACTTAGAAAAAAGAGTGAAGCAATTTGACCTGGTTTAACAATTTGGCTCTTGGACTCATTTGGCCACACTTATTTGCAAGAACAGTTAAAGCAGCATA
Ba13	TACATGTCACTATCGAAACAAAACTAGCGCAAAATCGGAAACCGGAGTGAACATAACAGGAAGCTGTTAATCGCGCTGTTTACTTTTCACTGCTTATGTCACGAGGAATTTGGTAAA

FIG.41-22

Ba14 TCAAAAGGAATTGTAATAGGTGATGGTCGGTGGGAACATTATTACATTCACACGGTTTGCAAAGTAGTTTGAAGAAATGAATATATCTGATCCAGATTTAATTATATCGATTTCATAAG
Ba15 AATTAGGATGAGTCCGTACAATATATACAAATTACTGTAGGAGGTTTACCACATGACAAAAACGTCATCTGTTACATCTGAGTCTGTAACCTGAAGGACATCCAGATAAAATTTGT
Ba16 ACGGTGGCTACCGTATCAAAAATTAAGGAGTCAATCAAAAATCTAGCTCAGCGGTAGAACAGTCGGTCTGTTTCATCCCTTCCATGAGGCAAAAAGCGGCTCTAAGTCTG
Ba17 GGAAGGAACGATTTGTGTCAAGGTGGCTATACGCCAAAGAAATGGAACACCGGTGTTTACCGCTTTATCAAGCACGACGTATAAATATGATACTTCGGATGATTTAGCAGCATTAAT
Bc01 GGGAAAAATGATTTCTTTTAAATGTAAGTAAGTATATGAACAGGTGGCAATCTGTTCAATGAGGAGTGAAGTAAATATCAATTTAGAGAAAAAGTGAAGAAAGTACGTTTA
Bc02 TGGTTGCCGATTTTGGGGATGGCTTCGGAAATGTAATGATGATCTATGCCGCTACGTTTGAGTATGCAAAACAAACGGCGCAGCGGAGCAAAATTAGGTTTTTCAACAAACACTT
Bc03 TTTGAGGAGTATCTGAGAAAAATGAAGCGATGCTTGCATGATAGAAATATGGTTCAATTTGCAAGATGGCAAGTCAATTTAGAGAAAAAGTGAAGAAAGTACGTTTA
Bc04 AAGAAACGAGAGGAAATGGTTTGGCATTTATACCACCTTGGGATATTTTGGGCTATTTATGGTTCTGGAATTTATACAGGTGATTTCTATAAAATGCGGATACTTGTAGCAATTTCAA
Bc05 AATATAGAGTAATAAAGTTGACTATTAGAGGGGAGAAATGTAATGAATAAATATCAACAAAAATAGTAGTGGCAATCGGAAATGGAGGACATTTACGGGATATTAGGACTTTGGG
Bc06 CGTCACAAAGAAAAACAATTTGAAGAGAGTATTGAAGAAAAATAGGAAAAAGTACATAGAAACAAGTCAAGATATTCATCGCAATCCGAGATTGGTAACCAAGATTTTACGCATCAAGAA
Bc07 TAGAAAGTTTCCGCAATTTAAGTATGTATACATAACTTTAGGAATTAAGTATGTTCAATGATTTCTTTGTTATAGGATAGGTTTGGCGATCATAAACGAAAAACAAAAACGA
Bc08 GGTGGGCAATTAAGTATGACACTCGAAAAATAGTCAAACTGGGTAGTACAGTTTATGAATATATGATAGAGCAAGATAAGCAATATCATTTGTAGATATTCAGAAACATATCGTTTCGC
Bc09 ATTTAATCCATGATTCACATAACTTAGAAAAAAGCTGAGCAAAATGCACTCGGTTAAGAAATGGCTCTTGGACTCATTTGCCACATTTATTTGCAAGAACAAATTTAAGCAGCATA
Bc10 TCAAAAGGAAATGTAATAGGTGATGGTGGGCTTATACATTCACATGGTTTACAAAGTAGTTTGAAGAAATGAATATCTGATCCAGATTTAATTATATCGATTCATAAG
Bc11 ACATGTCAACTATCGAAACAAAAATAGCGCAAAATCGGAAACCGGAGTGAACACTACAACGGAAGTGAATCCACCTGTTTATTTTCAACTGCTTATCGTCAGGAAGGAAATTTGGTAAAT
Bc12 GGGATATTAATGCAATTAAGTGAACAAACAGCTATACAAATATGCGAAAGAACACGGTTTATTTGAAAGAAAGCAAAATGTTTGTGATGAAATGGAGATGGAAAAATTTAAATACGTGTT
Bc13 AATTAGGATGAGTTCCGTACAATATATACAAATTAAGTGAACAAACAGCTATACCAATGATTTCTATTAGAGAAATGAAGAAAAATATATAAGCAAAAAAGCGGTGAT
Bc14 ACGGTGGACTACACGCAATTAACATAAAAAATTCGGAGTCGATCCAAACAAAAAAGGGGTGATACACCAATGATTTCTATTAGAGAAATGAAGAAAAATATATAAGCAAAAAAGCGGTGAT
Bc15 GGAAGGAACAAATTTGGTGCAGGTTGGCTATACGCCAAAGAAATGGTGAACCGGTGTTTACCGCTTTATCAAGTACAGGTATAAATAGGATACTTCGGATGATTTAGCAGCTTAT
Bc16 GAAAAATCAAAATGAAAAAAGTTTGTACCCGTTATGATCAGTTGTAGGAGTAAGTATTTTAACTGGTTGGGTAGTTTAAAAACGAAAGCAAGCGGAGCAAAATGCAAAAGACGAG
Bc17 TATTAGCATTGTAAGTGGGCTGTATTATTAAAGCGCATGTAGCGGAGTTAGATGAAGAAAAAGATTACTGTGGTGTAAACAGGAGGCGCTCATG
Bc18 AAACCTAAGTAATATATGTTTAGGGGTTATTGGAGTGTATGTAATTAATAAATTAATCAGTTATGGTTTACGCTATGGGTTATTACGAGGTGACATTTCTAATTATGCAATATAT

FIG.41-23

B. Cobalamin Riboswitch Alignment.

ID		Start	End	Accession	Organism
Atu01	+	70441	70625	NC_003304.1	Agrobacterium tumefaciens
Atu02	-	441331	441136	NC_003305.1	Agrobacterium tumefaciens
Atu03	+	877645	877833	NC_003304.1	Agrobacterium tumefaciens
Atu04	+	921717	921886	NC_003305.1	Agrobacterium tumefaciens
Atu05	-	1640563	1640420	NC_003304.1	Agrobacterium tumefaciens
Atu06	-	2810076	2809899	NC_003304.1	Agrobacterium tumefaciens
Bha01	-	466904	466746	NC_002570.1	Bacillus halodurans
Bha02	+	528894	529051	NC_002570.1	Bacillus halodurans
Bha03	+	870599	870748	NC_002570.1	Bacillus halodurans
Bha04	+	1661078	1661219	NC_002570.1	Bacillus halodurans
Bsu01	-	3403719	3403620	NC_000964.1	Bacillus subtilis
Bja01	+	2232813	2232975	NC_004463.1	Bradyrhizobium japonicum
Bja02	+	3617311	3617490	NC_004463.1	Bradyrhizobium japonicum
Bja03	+	3630677	3630857	NC_004463.1	Bradyrhizobium japonicum
Bja04	+	3634122	3634284	NC_004463.1	Bradyrhizobium japonicum
Bja05	-	5279669	5279495	NC_004463.1	Bradyrhizobium japonicum
Bme01	+	679030	679218	NC_003317.1	Brucella melitensis chromosome I
Bme02	+	717388	717585	NC_003317.1	Brucella melitensis chromosome I

FIG.41-24

Bme03	+	559758	559950	NC_003318.1	Brucella melitensis chromosome II
Bme04	-	973106	972933	NC_003318.1	Brucella melitensis chromosome II
Ccr01	+	502968	503156	NC_002696.2	Caulobacter crescentus
Ccr02	+	1925017	1925166	NC_002696.2	Caulobacter crescentus
Cte01	-	409802	409630	NC_002932.3	Chlorobium tepidum
Cte02	+	422045	422244	NC_002932.3	Chlorobium tepidum
Cte03	+	443769	443951	NC_002932.3	Chlorobium tepidum
Cte04	+	584183	584411	NC_002932.3	Chlorobium tepidum
Cte05	+	882576	882770	NC_002932.3	Chlorobium tepidum
Cac01	+	1509969	1510116	NC_003030.1	Clostridium acetobutylicum
Cac02	+	2557903	2558041	NC_003030.1	Clostridium acetobutylicum
Cpe01	+	248269	248429	NC_003366.1	Clostridium perfringens
Cpe02	+	1241749	1241887	NC_003366.1	Clostridium perfringens
Cpe03	-	1431291	1431152	NC_003366.1	Clostridium perfringens
Cpe04	-	1549481	1549348	NC_003366.1	Clostridium perfringens
Eco01	+	4160983	4161133	NC_000913.1	Escherichia coli
Fnu01	+	934517	934658	NC_003454.1	Fusobacterium nucleatum
Lig01	+	1347854	1347994	NC_004342.1	Leptospira interrogans chromosome I
Lmo01	+	1179829	1179979	NC_003210.1	Listeria monocytogenes
Mlo01	-	1101076	1100918	NC_002678.1	Mesorhizobium loti

FIG.41-25

Mlo02	+	1149143	1149308	NC_002678.1	Mesorhizobium loti
Mlo03	-	4044577	4044416	NC_002678.1	Mesorhizobium loti
Mlo04	-	4957334	4957164	NC_002678.1	Mesorhizobium loti
Mlo05	-	6170855	6170715	NC_002678.1	Mesorhizobium loti
Mlo06	+	6749148	6749315	NC_002678.1	Mesorhizobium loti
Mle01	-	1130394	1130222	NC_002677.1	Mycobacterium leprae
Mtu01	-	309822	309703	NC_000962.1	Mycobacterium tuberculosis
Mtu02	-	1261701	1261497	NC_000962.1	Mycobacterium tuberculosis
Pae01	+	1381520	1381688	NC_002516.1	Pseudomonas aeruginosa
Pae02	-	3261415	3261204	NC_002516.1	Pseudomonas aeruginosa
Pae03	+	3265563	3265728	NC_002516.1	Pseudomonas aeruginosa

FIG.41-26

ID		Start	End	Accession	Organism
Pae04	-	3305780	3305629	NC_002516.1	<i>Pseudomonas aeruginosa</i>
Ppu01	-	2765203	2765045	NC_002947.3	<i>Pseudomonas putida</i>
Ppu02	-	2768953	2768785	NC_002947.3	<i>Pseudomonas putida</i>
Ppu03	+	3857563	3857746	NC_002947.3	<i>Pseudomonas putida</i>
Ppu04	-	3981958	3981816	NC_002947.3	<i>Pseudomonas putida</i>
Rso01	-	2609233	2609017	NC_003295.1	<i>Ralstonia solanacearum</i>
Sne01	+	954780	954943	NC_003047.1	<i>Sinorhizobium meliloti</i>
Sne02	-	1999747	1999574	NC_003047.1	<i>Sinorhizobium meliloti</i>
Sne03	-	2122891	2122516	NC_003047.1	<i>Sinorhizobium meliloti</i>
Sne04	+	66265	66456	NC_003078.1	<i>Sinorhizobium meliloti</i> plasmid pSymb
Sne05	+	580403	580578	NC_003078.1	<i>Sinorhizobium meliloti</i> plasmid pSymb
Sco01	+	1037869	1038053	NC_003888.1	<i>Streptomyces coelicolor</i>
Sco02	+	1045899	1046106	NC_003888.1	<i>Streptomyces coelicolor</i>
Sco03	+	1051420	1051563	NC_003888.1	<i>Streptomyces coelicolor</i>
Sco04	-	5688395	5688291	NC_003888.1	<i>Streptomyces coelicolor</i>
Sco05	-	6532337	6532191	NC_003888.1	<i>Streptomyces coelicolor</i>
Sfl01	+	4183416	4183566	NC_004337.1	<i>Shigella flexneri</i> (*)
Son01	+	826836	827026	NC_004347.1	<i>Shewanella oneidensis</i>

FIG.41-27

Son02	+	1071692	1071874	NC_004347.1	Shewanella oneidensis
Sti01	-	2114053	2113918	NC_003197.1	Salmonella typhimurium
Sti02	+	4347871	4348024	NC_003197.1	Salmonella typhimurium
Tma01	-	84288	84144	NC_000853.1	Thermotoga maritima
Tte01	+	395153	395353	NC_003869.1	Thermoanaerobacter tengcongensis
Tte02	+	396075	396275	NC_003869.1	Thermoanaerobacter tengcongensis (*)
Vch01	+	145142	145306	NC_002505.1	Vibrio cholerae chromosome I
Vvu01	+	1165724	1165882	NC_004459.1	Vibrio vulnificus chromosome I
Xac01	-	3631166	3630987	NC_003902.1	Xanthomonas campestris
Xax01	-	3758428	3758245	NC_003919.1	Xanthomonas citri
Ype01	-	4393235	4393008	NC_003143.1	Yersinia pestis
Aca01	-	340	170	M34485.1	Acinetobacter calcoaceticus
Avi01	-	388	214	U45329.1	Agrobacterium vitis
Bfr01	+	580	762	AY043208.1	Bacteroides fragilis
Bmg01	+	1211	1350	AJ000758.1	Bacillus megaterium
Lma01	-	76392	76234	AL499620.1	Leishmania major
Pfr01	-	543	373	AY033236.1	Propionibacterium freudenreichii
Rca01	+	105327	105521	AF010496.1	Rhodobacter capsulatus
Rca02	+	116991	117174	AF010496.1	Rhodobacter capsulatus
Rca03	-	39849	39672	AF010496.1	Rhodobacter capsulatus

FIG.41-28

Rsp01	+	201	341	B07728.1	Rhodobacter sphaeroides
Sbi01	-	330	147	BH245584.1	Sorghum bicolor
Sgi01	-	9209	9035	AF263012.1	Streptomyces griseus
Svi01	-	1235	1052	U27616.3	Stealth virus 1
Zmo01	-	24942	24808	AF193754.1	Zymomonas mobilis
Zmo02	-	4323	4162	AF193754.1	Zymomonas mobilis

Accession numbers are for Genbank sequence entries. Start and end positions are the 5' and 3' nucleotides of the first interior UG base pair of stem P1 (orange). Secondary structure (SS) and sequence consensus (Cons) lines are shown above the alignment. In the consensus sequence, uppercase and lowercase letters represent =90% and =80% conservation at a position, respectively. The degenerate bases R (A,G) and Y (C,U) appear only when a single base is not 80% conserved. Sequences marked with an asterisk (*) were excluded when determining the sequence consensus because they have >90% identity to another sequence in the alignment.

FIG.41-29

Pae04	CGUAGCCUUGCCGGUUGAGGUU	CCUUGCGCG	GGCA	GGCGGGG	CU	AAGA	GGGAAC	GGCGUUG	---	AUG			
Ppu01	GUUACCAUGCGGGCCGCGGU	UUCG	ACCAC	GGAA	CU	AACA	GGGAU	CCCA	GGCUUG	CCAAUA	CAGGCG	AA	
Ppu02	CAGAUGCGCCAGUUCAGGUG	CCUUGGGG	CGCCGC	GGCAGGG	UG	AAAC	GGGAA	CGCGUGG	UUGGUG	UUGCC	CACGAG	AAGU	
Ppu03	UCCUUAUGCCUUGCGGUUCAGGUG	CCCG	UCAG	GGGG	UG	AAAC	GGGAA	CGCGUGG	UUCG	GGCCCU	UCAGC	AGGGCCGGAG	AUUG
Ppu04	CGUAGCCUUGCCACUUCGAGGUU	CUUUGGG	CUG	GGCGAAG	CU	AAGA	GGGAAC	GGCGUAC	---	---	---	AAG	
Rso01	GUUACACUUGCCGGGUCCUGGUG	CGCAGA	CGCGA	UUGGAG	UU	AAAC	GGGAAG	CAGGAG	CGCGCGG	CCAAAC	GGUGCG	CCAA	
Sme01	CUUAGAGAGGACACUCAAGGUG	CGGCCUG	GAAG	GGAGGGGG	AG	AAUJ	GGGAAG	CGCGUCA	---	---	---	AAUC	
Sme02	UGGCCAUUAGCCGCCGUCAGGUG	CCCGG	GAAAU	GGGGGG	AG	AAUJ	GGGAAG	CGCGUGC	---	---	---	AGUU	
Sme03	UAAUUAACGACAGUAGGAGGUU	UUCUUGG	GAGGU	GGGAGGGAG	GU	AAAU	GGGAUJ	GGGAAGG	GGGAG	CGG	ACGCC	GGGGCGCUUA	
Sme04	CACAUUAACUGGGACCGAGGUG	UCCCGU	GUGA	GGGAGGGG	UU	AAUA	GGGAAC	ACCGUGCG	ACGAG	CGG	AAGA	GGGAG	AAAA
Sme05	GCAUACCAUACUAGUGAGGUG	UCCCGG	CGACUGAAGAAC	GGCGGAG	UG	AAAA	GGGAAC	ACCGUGAG	GGAGAG	CGG	AUCA	GGGAG	AAAA
Sco01	UAGGUGGCCCGUGCAGUUGGUU	GGCCCGG	GCCA	GGCGGAGU	GG	GGCAAG	GGGAAC	CGCGUGG	---	---	---	GAUU	
Sco02	UAGGUGAGCCCGCAGUUGGU	UCCCGG	GAUCA	GGGAGGG	GG	GGCAAG	GGGAAC	CGCGUGG	---	---	---	GAUU	
Sco03	GCAGACGUGAGUACAGCGGUG	CUUCG	CCG	GGGAGGG	GG	GGCAAG	GGGAAC	CGCGUGU	---	---	---	GAUU	
Sco04	UAGGUGAGGUGGUGGUGGUG	UUCG	CCG	GGGAGGG	GG	GGCAAG	GGGAAC	CGCGUGC	---	---	---	GAUU	
Sco05	ACUAGUGGCCAGCGUUGGU	UUCG	CCG	GGGAGGG	GG	GGCAAG	GGGAAC	CGCGUGU	---	---	---	GAUU	
Sf101	CCUAGAGCAUCCAUUGCGGUG	UUCG	GUG	GGGAGGG	GG	GGCAAG	GGGAAC	CGCGUGC	---	---	---	GAUU	
Son01	UUUAGAGUACACCUUCUGGUG	UUCG	AUAG	GGGAGGG	GG	GGCAAG	GGGAAC	CGCGUGA	---	---	---	GAUU	
Son02	ACUAGUGUUAUGCAUAGGUG	UUCG	AUAG	GGGAGGG	GG	GGCAAG	GGGAAC	CGCGUGA	---	---	---	GAUU	
Sti01	GCCAUACGUAACCAACAGGUG	UUCG	AUAG	GGGAGGG	GG	GGCAAG	GGGAAC	CGCGUGA	---	---	---	GAUU	
Sti02	ACGAGAGCAUCCAUUGCGGUG	UUCG	AUAG	GGGAGGG	GG	GGCAAG	GGGAAC	CGCGUGA	---	---	---	GAUU	
Tma01	GAAGCCUCCUACCGUGCGGU	UUCG	AUAG	GGGAGGG	GG	GGCAAG	GGGAAC	CGCGUGA	---	---	---	GAUU	
Tte01	UUGAAUUAAGCCUUAUGGU	UUCG	AUAG	GGGAGGG	GG	GGCAAG	GGGAAC	CGCGUGA	---	---	---	GAUU	
Tte02	UGAAUUAAGCCUUAUGGU	UUCG	AUAG	GGGAGGG	GG	GGCAAG	GGGAAC	CGCGUGA	---	---	---	GAUU	
Vch01	AUACUACAGCGCCAGCGGUG	UUCG	AUAG	GGGAGGG	GG	GGCAAG	GGGAAC	CGCGUGU	---	---	---	GAUU	
Vvu01	AUAGUAGCGGUUACAGCGGUG	UUCG	AUAG	GGGAGGG	GG	GGCAAG	GGGAAC	CGCGUGU	---	---	---	GAUU	
Xac01	CUACAUAGCGCGCCUAGGUG	UUCG	AUAG	GGGAGGG	GG	GGCAAG	GGGAAC	CGCGUGU	---	---	---	GAUU	
Xax01	CUACAUAGCGCGCCUAGGUG	UUCG	AUAG	GGGAGGG	GG	GGCAAG	GGGAAC	CGCGUGU	---	---	---	GAUU	
Ype01	UACUAGUGGAGCAUUGGUGGUG	UUCG	AUAG	GGGAGGG	GG	GGCAAG	GGGAAC	CGCGUGU	---	---	---	GAUU	
Aca01	CUUACACAAUUCGUAACAGUUA	UUCG	AUAG	GGGAGGG	GG	GGCAAG	GGGAAC	CGCGUGC	---	---	---	GAUU	

FIG.41-32

Avr01	CCUAAAGUGGCAGCCUAUCCGU	UCUGCAACUGU	CAAA	ACCGUCCGGAGUG	AAA- GCGAAU- ACCGUGACGGACGACCG	AAGUAA	CGGCGGAAA
Bfr01	UUUAUUUUGUCUCCUGAUGCGU	UCCGAAUAG	UCAUCCU	CUAU	CGCAU- AAA- GCGAAU- CCGGUGU		AAAU
Bmg01	AUCAAAACAGCAACAGUAAAGGU	GGU	AAGAA	EGGU	AAUA- GCGAAA- CUGGUGA		AAGA
Lma01	-----UCCGGUG-----	CCCU	UCAC	ACGGUG	AAAC- GCGAAA- CCGGUGACUUAUGU	CCUUUACUUAAGGCGGUGACGAGU	
Pfr01	UGUGUAGGCUAGUAGUGGUGU	CGGUGGGU	CCAC	GGCAGUGG	CGCAAG- GCGAAU- CCGGUGU		AAUU
Rca01	GGCACUCAGGCGGCGGCGUGGU	UCUGUG	CUAU	CACAGGUG	AACA- GCGAAU- GUGAAGGAAUUG	CGGCGGAAUCCCGA	
Rca02	GGCUACUCCAAACAGCGGAGUGU	UCCG	AACUGGAC	GGCAU	AAUA- GCGAAC- ACCGUGACGUAUUAUCCG	AUCA	CGGCGGAAU
Rca03	GGGCACCUUGCGCGGCGAGUGGU	CGGCGGAAACG	CAC	GGCGCGGUG	AAA- GCGAAU- ACCGUGUGGUAUUAUCCG	AUCA	CGGCGGAAU
Rsp01	UGUUUUGGCGAGGCGGUGACGNG	CGGCGG	UUUG	CGCGGAG	AAUC- GCGAAG- CCGGUGG		AAAU
Sbi01	UAGACUGCGGCCACUUCAGGUG	ACUUGCGG	CAUG	CGCAGGUG	AAAC- GG- AAC- CCGGUGACCGGUG	AUUC	CACCGCAGG
Sgi01	UAGGUGACCGGUGGACGUGGU	CGGCGGUGG	GCCA	CGCAGGUG	CGCAAG- CCGGUGG		AAAU
Svi01	AUCCUGGCUUACAGGAAACGGU	UCUGGGU	GAGA	GGUGGAG	AAA- GCGAAC- ACCGUGACGCA	UUAAAU	UGCUCAUG
Zmo01	CGGAAAUUUUUUGCAUAGGU	UUCCUUG	GAGU	CAAGGAA	AAUU- GCGAAC- AAGGUGG		AAAA
Zmo02	AGCAUAGCAAGCAUUAAGGU	CUUUGU	CAUUG	CAAAAGCU	AACA- GCGAAA- CUGGUGGCAAA	GAAU	UUUCAAAG

FIG.41-33

Atu01	CGAAGACUGCCCGCAACUGUGA-GCGG	CGAGCAUGUUCGGAUUG
Atu02	CUUGGCUUGCCCGCAACUGUAA-GCGGAUJ	GUUGUICAUCCCAUGAGCGCUUGAAEGCGUCAL
Atu03	UGGUGGCUUGCCCGCAACUGUGA-GCGG	AGAGCCUGAAGGAUUGCCACUGGCAA
Atu04	CCGAGGCUUGCCCGCAACUGUAA-GCG	ACAGCGAAAGUCCAUCAU
Atu05	CCGGAACGUG-CCCAACGUGUAA-GGC	GGAUUGCUUUUUCALU
Atu06	CCGUGGCUUGCCCGCAACUGUAA-GCGGU	AAGCCCGCACCGUAAA
Bha01	CCGAGCGGCUCC-GCCACUGUCA-UAGC	UGAGUUGUAAGAUUU
Bha02	CCGAGGCUUGCCCGCAACUGUGA-GUGCU	ACGAACGGAACGAUUU
Bha03	CCAGACGGU-CCGCGCACUGUAUAGG	AGCUACAUUGAGGAA
Bha04	CCGAGACGGU-CCGCGCACUGUAA-AUG	GGAGAGGUUGCAAGA
Bsu01	CCGUGGCU-CCGCGCACUGUAA-UUGGC	
Bja01	CCGCGCUUGCCCGCAACUGUGA-GCGG	CGAGCCGUGUCCGACGAU
Bja02	U-GCAGCGCCCGCCGACCGUGACCGGAG	AGAUGCCCGAG
Bja03	CCCAAGCGCCCGCCGACUGUAA-GCGGU	GAGGGGCUCCGAACC
Bja04	CCGCGGCUUGCCCGCAACUGUAA-GCGG	AUAUCCUUGUGACAA
Bja05	CCAGGCUUGCCCGCAACUGUAA-GCGG	UGAAUUCUUUGUCAAU
Bme01	CCGAGACUGCCCGCGCAACUGUAA-GCGG	AGAGCUAUCUCCACAECCGCGGCAAECCGGCAAA
Bme02	UCCGACGCCACCCCGCACUGUAGCGG	AGAGGGAAGAGGCAAECCGCGCAAECCGGCA
Bme03	CCGUGGCUUGCCCGCAACUGUAA-GCGGA	UUGCCGCUAUCUUGUGACCGCGAAEEGUCAL
Bme04	CCGAGGCUUGCCCGCAACUGUAA-GCGGC	GAGCUUUGGCCCCAU
Ccr01	CCGCGGCUUGCCCGCAACUGUGA-GCGG	CGAGCCGCUUGCCGUUCGU
Ccr02	CUUGGCUUGCCCGCAACUGUAA-GCGG	CGAGCUUGCGUACA
Cte01	CCGGAACAGUACCGGCUUGUGUAA-UUCG	GGUGGCGCAAECCUGGCGACAAGGUUUGCCGACAAU
Cte02	CGUACACUGUACCGGCAACUGUACACGGU	UAAECCGCGCGCAACCGAUUGGGAEEGCGEQUUCAG
Cte03	CCGGACAGUUGCCGCUUGUGUGA-UCCUC	CCGUGGCGCACAUUGCCGCGGAGAUUGGUGAUGA
Cte04	CGCAACUGUGCCGCAACUGUAA-GAUGGU	AUGUGCGCGAGGAGGCAEQUUGCUUUUGUGUGGGAUUGGUGUUAU
Cte05	CGUACACUGUACCGGCAACUGUACACGG	AAAAUGUGCGUGGUAUGCCCAUGCCUCAAAGCGGACGCGGUGCAC

FIG. 41-34

Cac01	CCUGACGGGU-CCCCGCCUGUAUAUAGG	ACUUUAAGUACAAUAU
Cac02	CCAAUUGCAACCCCGUUAUACUGUAU-ACAGUU	ACAAAACCAADG
Cpe01	CCCACGGGGU-CCCCGGCGUGUA-UAG	AGGACUUUUUGUACUUUA
Cpe02	CUUCAACUACUCUACUACUACUGAAGC	AGACAAAUUCUAAUAU
Cpe03	CCACUAGGCGCGCGUACUGUAGG	AUACAGUUUCUUAUUCA
Cpe04	AAUUGCAGCCCCCGUACUGUG-AUAAG	CACGAGAUAAAG
Eco01	CUUGAGCUCA-CGCGCAGCGUA-CCA	AAGUGCGAUGAUUCGUAUCCG
Fnu01	CCAAAACGAG-CCUUGCGUGUAUUA	GUUUUUUUCUUGUUUA
Li g01	CCGCGACUGAACCCGACUGUA-UCCCGCA	AUGAGAUUUGCGAAUCAU
Lmo01	CCGAAACUGCCCCCGCAUCUGUA-GGU	GCACAAGAUCCAGAU
Ml o01	CCGUGGCUUGCCCCCGCAUCUGUG-GCGG	UAGUCCUUCUCCAUU
Ml o02	CCGCGCGUGUCCCCCGCAUCUGUA-GCG	AAGAGCCAAAGCGCGAAAG
Ml o03	CCGCGCGUGUCCCCCGCAACGGUGG-UGGAG	UUCAGUCCGAACGGGAG
Ml o04	CCGCGCGUGUCCCCCGCAACUGUA-GCGG	CGAGCCAAAGCCAUUGGU
Ml o05	CCGUGGCGUG-CCCAAGCGUGUA-GGGG	CACCCCGCGCGUAAAU
Ml o06	CCGUGGCGUGCCCCCGCAACUGUA-GCGG	AGAGCAAGAUCCACA
Ml e01	CCGCGACUGU-CCGCGAGCGUAU-GCAGG	AAGACCGCGGUGUGGAA
Mtu01	CCGCGCGGGU-CCCGCCACUGUA-CCGGG	CAGCGACCCUUGUA
Mtu02	CCCGAUUGU-CCGCGAGCGUAU-GCAGG	AACCGCGCGUUGGAGUAGACAA
Pae01	CCAGCGUGCGCGCGCAAGGUAU-GCGA	AUCAGACAGCGCGGUAUA
Pae02	CCGUGGCGUGCCCCCGCAACUGUAU-GCAGCCUG	UAUUGCGCGCAUUC
Pae03	CCGCGCGUGCCCCCGCAACGGUAU-GCGAG	CGAAAUCCUUCUUCAG

FIG.41-35

Pae04	CCGCGGCTUGCCCGCCGCAACUGUGA-ACGG	CGAUGGUUCCGCAAU
Ppu01	UUGGAACUGCCCGCCGCAACUGAG-GUCC	CGACCCUGCTCCAUCCAU
Ppu02	CCCGUGCTUGCCCGCCGCAACGGUAA-GCCAG	CGAACCCUUGCGAGU
Ppu03	CCCGUGCTUGCCCGCCGCAACGGUAA-GCCAG	UGAAGCGUCUGU
Ppu04	CCCGGCTUGCCCGCCGCAACUGUAA-GCAACG	ACAACGGAUCCACACA
Rso01	CUUGCCCTUGCCCGCCGCAACGGUAAACCGCGU	UCCCGCAGUCCGUGCCACAU
Sme01	CCGGGCTUGCCCGCCGCAACGGUGG-UGGAGC	GAACAGCCACGGCACAAG
Sme02	CCGGCAGCTUG-CCCAACCGUGUAGAGG	GACGUCUCCGCAAAAAGGCUUCUGAAUCUUCAGACCUUU
Sme03	UUGCAGCCGACCCCGCCGCAACUGUAGACGGU	CAGCGUCCGCAUUGCGCAUUGCGCGGAUUUCAUCCGCTUGGUGCGG
Sme04	CCGUGCTUGCCCGCCGCAACUGUAGCGGAU	CGUGGUCAUCCUUGUGCGGCAAGCGGCA
Sme05	CCGUGCTUGCCCGCCGCAACUGUGA-GCGG	CGACCAAGUCCACGGAU
Sco01	CCGGGACTUG-CCCGCAGCGGUGA-GCGGG	AACGACCGCGGUGAUA
Sco02	CCGGGACTUG-CCCGCAGCGGUGA-GUGGG	AACCAAGCGGUGAACA
Sco03	CCGGCAGCTUGCC-GCAACUGUGA-GCGGG	CAGUCCACCCUUGCAGAC
Sco04	CCGGAACTUG-CCCGCAACGGUGU-AC	UUGCGUGCAUC
Sco05	CCGUGCTUGCCCGCCGCAACUGUGA-AUCCGG	UAGUCCGCTUGCCGCGUGACGCGA
Sfl01	CUAGACTUGA-CCCGCAGCGGUA-GGA	AAGGUGCGAUGAUUGCGUUAUCCG
Son01	CUGCCACTUGCCCGCCGCAACGGUAAAGGU	CACAGACCGCGCGCAUU
Son02	CCCGAACTUGUACCGCCGCAACUGUGA-GUAG	UUAAAGAGCGCGUAGAUU
Sti01	CCCGGCTUGCCCGCCGCAACUGUGA-GUCC	UGACCGCCCGUAAAGA
Sti02	CUCCGACTUGA-CCCGCAGCGGUA-GGA	AAGGUGAUGACAGCGUAAAGCA
Tma01	CCCGGCGGGG-CCCGCAACGGUGA-CGGGG	CACCAACCGCGCAGAAC
Tte01	CCCGGCGAGCCCGCCGCAACUGUGA-GGCA	GGACCAAGCCUAGUAA
Tte02	CCCGGCGAGCCCGCCGCAACUGUGA-GGCA	GGACCAAGCCUAGUAA
Vch01	CCCGAACTUGA-CCCGCAGCGGUA-GAGAG	AACGAACGCTCAAAC
Vvu01	CCCGAACTUGA-CCCGCAGCGGUAUAGAG	AACGAACGCTUAAUCA
Xac01	CCCGAGCTUGCCCGCCGCAACGGUGG-GCGAG	GUCAGUGCCGCAACAG
Xax01	CCCGAGCTUGCCCGCCGCAACGGUGG-GCGAG	GUCAGUGCCGCAACAG
Ype01	CCCGAACTUGA-CCCGCAGCGGUAAGCGGA	AGUCACCGCGCAUAGGUUUAAGU
Aca01	CCAGCTUGCCCGCCGCAACGGUAA-AAUUG	UAAACCAUUAUAAAGUUAUUAACAUUA

FIG.41-36

Avi01	CCGUGCGUGCCCCCGCAACUGUGA-ACGG	CCAGCGAUGUCCAUCAU-----
Bfr01	CCCGGACAGU-CCCGCUGCUGUGAAGCTCC	GUCUGAUUUCCCAUAACAAGTUU
Bmg01	CCAGUACUGCCCCCGCAACUGUAA-GUGUG	CACGAACGAGUAU-----
Lma01	CCCGUGCUGCCCCCGCAACUGUAA-GCGAG	UGAAGCGUCAAU-----
Pfr01	CCGGAACUGU-CCCGCAGCGGUCA-AUGGG	AACGACACAACGUAG-----
Rca01	CCGCAAGCGCCCCCGCAACUGUACCGGA	GAGGGCGCGCGCAG-----
Rca02	CCGUGCGUGCCCCCGCAACUGUGA-GCGG	CCAGACGACGCGUGAAG-----
Rca03	CCGUACUGCCCCCGCAACUGUAA-GCGG	CCAGCACCCCCCGCA-----
Rsp01	CCCGCGCGGG-CCCGCGCGUGUGA-CGG	GGAUUGCUCGCGGCAAGAG-----
Sbi01	CCGGCGUGCCCCCGCAACGGUAA-GCAAGUC	AGUCCAGCGCAACAAC-----
Sgi01	CCCGGACUGC-CCCGCAGCGUGA-GUGGG	AACGACCGCGUGUA-----
Svi01	CCGAGACUGCCCCCGCAACUGUAA-CGGG	AGAGUCAUCCUCCUGAUGCUAUCUUAACGAUUAUA
Zmo01	CCUUGCGUGCCCCUGCAACUGUAA-ACAGU	UGAAACCGCAAAA-----
Zmo02	CCAGUGUGCCCCCGCAACUGUAA-ACGG	CCAGCAAAAGAUCAAAU-----

FIG.41-37

FIG. 41-38

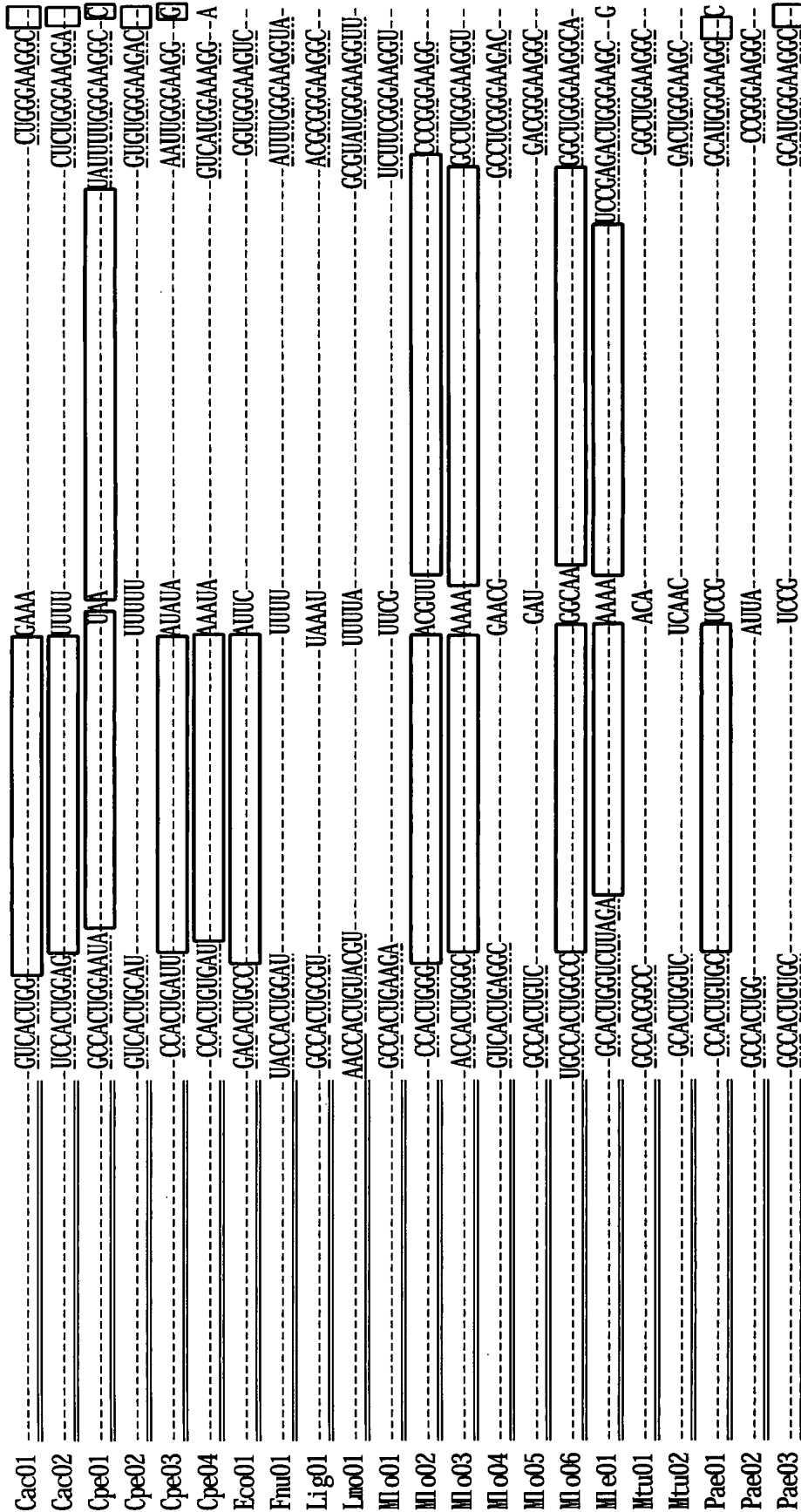


FIG.41-39

Pae04	GGACUGGG	UGA	CGCGGGAAGGC
Ppu01	GGACUGGG	CUGCC	CGCGGGAAGGC-C
Ppu02	ACCAUGUGG	UCAA	GCAUGGGAAGGU
Ppu03	ACCAUGUGG	UGUAGUAC	GCAUGGGAAGGU
Ppu04	GGACUGGG	CAAC	CGCGGGAAGGC
Rso01	GGACUGUUC	CGCG	GAAOGGGAAGGC
Sme01	GGACUGGAC	ACCGC	GUOCGGGAAGGC
Sme02	GGACUGAAUA	UUGAAGC	UAUUGGGAAGGC
Sme03	GGACUGGGGCAUUGCCAUUGCCAUACGCCGGGAGGAGCCUCUUCUUCUACCAUUGCUCGCCUUCUUGCCGAAACGCCGGAAGGCCA		
Sme04	GGACUGGGC	GGUU	CGCGGGAAGGC-A
Sme05	GGCAUUGGC	AUGAUC	GGCUGUAAGGC
Sco01	GGACUGGGGGC	ACGUAC	GGGGGGGGGAAGGC
Sco02	GGACUGGGGGCCAG	AUGAG	UUUGAGCGCGGAAGC
Sco03	GGACUGGGC	GC	CGCGGGAAGGC
Sco04	GGUAGGU	CUUCC	ACGUGGC-C
Sco05	GGACUGGUAUG	CUUG	CGGUGCGGAAGGC
Sfl01	GACACUGCC	AUCC	GGUGGGAAGUC
Son01	CGAUGGUGUUC	ACGAU	GAAOCCTUAAAUCC
Son02	CUAGAUCUAGAUCUAG	AUU	CUAGAUCUAGAUCUAAAG-C
Sti01	CCACUGAUC	GCA	GAUUGGGAAGC
Sti02	GACACUGCC	JCC	GGCGGGAAGUC-A
Tma01	GGACUGGG	CGAUCA	CGCUGGGAAGGC
Tte01	GGACUCUGCCCGGACUCACUCAGCCCG	UUAGUAAGGAGAAAGAGGGAGAGAAAU	UGCCUUCAGUUGAGUCCCGCUGGGAAGGC
Tte02	GGACUCUGCCCGGACUCACUCAGCCCG	UUAGUAAGGAGAAAGAGGGAGAGAAAU	UGCCUUCAGUUGAGUCCCGCAUGGGAAGGC
Vch01	GACACUGCU	UUUGC	AGUGGGAAGUC
Vvu01	GACACUGCAAGAU	GGA	AUCUUGGGAAGUC
Xac01	GGACUGUGG	JACAC	GCAUGGGAAGGC
Xax01	GGACUGUGC	AGUC	GCAUGGGAAGGC
Ype01	GGACUCUGCC	JCAA	GCAUGGGAAGUC

FIG.41-40

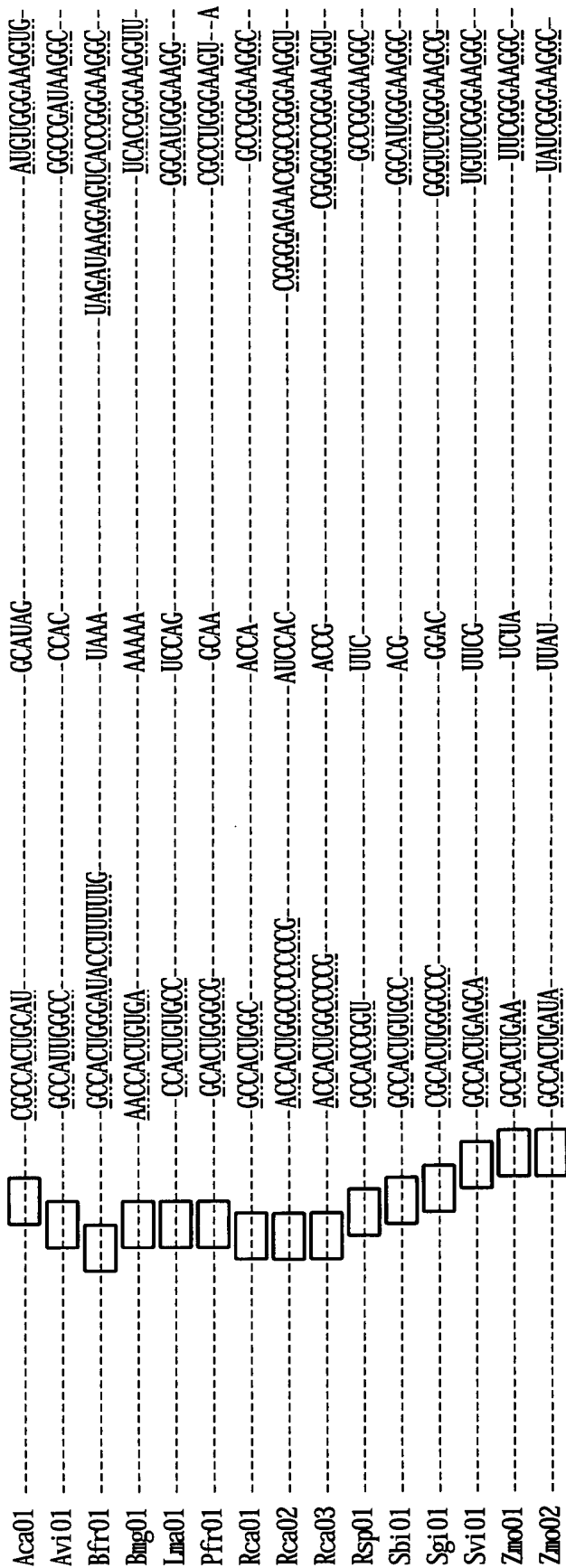


FIG.41-41

SS	y y	RAGYC	GRAGACC	GCC
Cons				
Atu01	GAUUGCAUGUUGUAG	CCCC	AAUUCAGCAGACCTUGCCUUCAGCGGAAAUUGUCCACG	
Atu02	CAUACAGACACCGA	AAUCCGU	GAGCCAGCAGACCTUGCCGUCAAAAUUGGAAACCAUCCG	
Atu03	UGCCCGAAGCGUUCAGGUUUCAG	CCGU	AA GCCAGCAGACCTUGCCAUACCGCAAAUUAUCCAUCCG	
Atu04	GCACCAAGCTUAGACC	CCG	AA GCCAGCAGACCTUGCCGGCAUACAUAAACGUCCACG	
Atu05	CAAAAGCGCGGAAGAA	CGU	UAGUCAGAGACCGGCCUUGCCAGCAUAGACCGCAAC	
Atu06	CGUCACAGCGUUGAUA	CGCGC	AAGCCAGCAGACCTUGCCGUUUCAGCAAAAAGCGUCU	
Bha01	UGUUGCAAUGUUGAC	GGUA	GAGCCAGCAGACCTUGCCUGUUCUAAACAGCAGUCGUU	
Bha02	UUCUAAGCUAGCUAA	AGCAC	GAGUCAGCAGACCTUGCCUUCUACUUCACAAAGUUCGC	
Bha03	CACAUCCAGUUGA	UCUU	AAGUCAGCAGACCTUGCCUAAUUGUAUUGCAGCUUGCAC	
Bha04	GCAAGUACUCCAUCAA	CAU	AAGUCAGCAGACCTUGCCUUCUUCAGUUCAGUGUGUAG	
Bsu01		GCCAA	GAGCCAGGAUAUCCUGCCUGUUCUACACAGCAGAAU	
Bj a01	CGCACAGACGCCAUGA	CCAGC	AAGCCAGCAGACCGCCCGCCGACAAUAUAUUGGUCCA	
Bj a02	GGGAUUGCAAGGGAAACCCU	CUCCG	CAAGCCGGCAGACCTUGCCAGCGCGGAGCGAAUUTUGGAC	
Bj a03	CGCAGAACCCACUGA	ACCCG	GAGCCAGCAGACCGGCCUGCCAUUUCUUCAGGCGCAA	
Bj a04	GACCAAGUUGUAGAC	CCGC	GAGCCAGCAGACCTUGCCGUACGCCUGGUGUACACAGC	
Bj a05	CAGTUAAGGUAAAGCAG	CCGC	GAGCCAGCAGACCTUGCCGUACAGCGUGUGUUCACAGC	
Bme01	GGAGCCAAAGCCAGAC	CCGC	AAGUCAGCAGACCTUGCCGUUUCUUCGUGUACCCAUUGCU	
Bme02	GCUUUAUCCCAAGAC	CCGC	GAGCCAGCAGACCTUGCCUGUUCGCAUUGAGGCGCAUUGC	
Bme03	CAUGACCGCGAUUA	UCCGC	AAGCCAGCAGACCTUGCCGUUCUUAAGUAGUCCAUUGU	
Bme04	GGCUGGAAGCGUUGA	CGCGU	GAGCCAGCAGACCTUGCCUUCAGCCUGAACGCUCCACG	
Ccr01	GGGACGGGUGACGAC	CCGU	GAGCCAGCAGACCTUGCCUUGCAGACAUAAACGUCCUCC	
Ccr02	GAGCCACAGAGCAUUGAC	CCGU	GAGCCAGCAGACCTUGCCGGGCGAGUGUGUUCAUUGCC	
Cte01	CGCCAGAUCC	CGCA	AAGUCAGAAAGACCTUGCCUUCAUUUUUUUGGCUUCGG	
Cte02	UUGGAGCGGCUCAU	CGCGU	AAAGUCAGCAGACCTUGCCAGUACGUAUUGCAGCCAA	
Cte03	GGAAGGCA	GGGA	GAGUCAGAAAGACCTUGCCGUAAUUGCAGUAAAUUGCUCC	
Cte04	UGCCCGAGGAAAGCUCAAGUAAUUUUGA	GCCAUC	GAAGUCAGCAGACCTUGCCGUAGUGUGUUGCGCCGGAU	
Cte05	UGCAUCC	CCGU	AAAGUCAGCAGACCTUGCCAGUUAUCUUCUUGCUUGCGAA	

FIG. 41-42

Cac01	GUACUUAAGCAUGA-----	UUUUU--GAGCCAGCAUACUUGCCAUUUCUAGUAUGUUUUU
Cac02	UGGUUGAGGCUA-----	AAUGU--GAGCCAGGAGACCUUACCUAAAUUUAUUGGAACUUC
Cpe01	ACAAAAGUGAUGAU-----	CUU--GAGCCAGAGACCUUGCCUUAUUUUUAAAACAUCAAGA
Cpe02	GAGAUUGGAGAGAA-----	GC--AAAGUUGGGAUUACCUUGCCUUUUUAUUUAAGUACUUAUA
Cpe03	AGAAUAGGCUAAG-----	CCU--UAUGUACAGAUACCUUGCCUAAAGAUCAUGAACUAGC
Cpe04	UUGUUUAGCAUGA-----	UUUAU--UAGCCAGGAGACCUUGCCUAGUAGCUUAUUUCUUAUUG
Eco01	AUCAUCUCUAGUAUGUACAUAGCC-----	UCC--AAGCCGGAACAACCUUGCCGGGCAAGCGUCCAUUCUGGU
Fnu01	AAGAAAUUAAA-----	UCA--UAAGUCAGAGACCUUGCAUAUUUGAAUUAUCUUAUCU
Lig01	UCCGAAA-----	UCCGCGA--AAGCCAGAGACCUUAAAGUAAAAAACAACUAA
Lmo01	CGAUUGUUGAUGAA-----	GGC--AAGUCAGGAUAUCUGCCAAUAUAAGAGCGAAGCAACU
MI o01	CGCGAAGGCGCCUGAU-----	CCGU--GAGCCAGGAGACCUUGCCGACGACCGGCAAAACUGACA
MI o02	CGGCACCCAGGCGAUGACC-----	CGC--GAGCCAGGAGACCUUGCCGUCUGCGACAAAAGAAUCC
MI o03	GUUGGACGCUUGCGCAAGGA-----	CUCCA--GAGCCGGAACAACGAGCGCGAGAUUUUUGAACUCGAC
MI o04	CGGCACAGGCUUGAC-----	CGGC--GAGCCAGGAGACCUUGCCGACGACCAACAGCUCCACG
MI o05	ACCGACGCGGCUUGA-----	UCCC--GAGCCAGAGACCGCGCCUGCGGAGGCAUCUUCUCCG
MI o06	CGAUUGGCGUAGAC-----	CGGC--GAGCCAGGAGACCUUGCGCAUCACUGAGUUGACCGGAC
MI e01	AUGGCCAUUACAAGCAUUAUCCAUUGGCG-----	CUUGC--GAGUCCGAAAGACCUUGCCGCGCUGUGUGCGGCGCGCGG
Mtu01	GAGGCAAGCAAGCA-----	UCCCG--GAGCCAGGAGACUUGCGGCUCAUCGCGUCCUCCACCC
Mtu02	GAGGCGCAUAGGAACACCGACCGGUGGAG-----	CUUGC--GAGUCCGAAAGACCUUGCGGCGGCGGCGGCGGCGCGG
Pae01	CGCGCUAGAGCGUACAGCGUUGC-----	UCCG--GAGCCCGGAGACCGGCGCUGACCGACCCACCGGCAUUG
Pae02	GGCGGAGAGCGAGUUGUUGCGCGGCGGCGGAGGCG-----	CGCGUCC--GAGCCAGGAGACCUUGCGGCGGAAACAGUCCCGAGU
Pae03	GAGGAUUAACAGAAC-----	CUUGC--AAGCCCGGAGACCGGCGCUGCAAGCGCCUUGUGGAC

FIG.41-43

[illegible]

FIG. 41-44

Avi01	GGACAAAGCCAGAC	CCGU	GAGCCAGGAGACCTUGCCGUAJAGCAUGGCGCGAAAGC
Bfr01	GUCCGAACAA	GGAGU	CAGUCAGAACACCTUGCCGCUUAUCAAAGCCUGUUC
Bmg01	CUCAGUAGAAUGA	UACAC	AAGUCAGGAGACCTUGUCUUAUUGAGGUUUGUUAU
Lma01	UGAUGCUUUAACAGCCACGCG	CUGGC	AAGCCCGGAGACCGGCGCGGAAAUACAUAACAA
Pfr01	GUAGUGGAGGAAGUCCGGAGUGAUCUCCGAAUG	CCCAU	GAGUCCGAACACCTUGCCAGCAGCCACAACAUCUGUU
Rca01	GGGGCCACCTUGAGGGGACCCGCCUUGGA	UCCG	CAAGCCGGGAGACCTUGCCAGCGAUGGAUUCGGGCG
Rca02	GACCCGAGUUGAUGAA	CCGC	AAGUCAGGAGACCTUGCCAUUGGCUUGGGGUGCGAAG
Rca03	GGGGAAGCCAGCAG	CCGC	AAGUCAGGAGACCTUGCCAUACGGCUCAUCAACCGCC
Rsp01	GGCGGGGGGAGAUAA	CCG	GAGCCAGAACACCGGCGCTUGACGAGAGGUUCCCGCC
Sbi01	GCUGGAGGUGGGUUGGCGCCACCG	GGCGGC	AAGCCCGGAGACCGGCGCGGAGGCUACAGGUCCGGA
Sgi01	ACGGCCACUAGGUUUGUUGGCGGCGCAGAGUG	CCCGC	GAGUCCGAACACCTUGCCCGCGCGCGCACCGGACCG
Svi01	GCAGGACCGAUGAAGAC	CCCG	AAGUCAGGAGACCTUGCCGCUAUGCCAGUACCCCAUGGC
Zmo01	GGUUGUUGGAU	CCUGU	GAGCCAGGAGACCGGACCCUAUGUAUGGUUCCACGA
Zmo02	UGAUGGAGCCCGUGAC	CCGU	CAAGUCAGGAGACCTUGCCUUAACCAAGUACAUCACU

FIG.41-45

C. C-Box

NC_002570.1/648448-648540	ACATGTAGATATCATCCCTTTCCTGtataTACTTGGAGataagg. TCCAGGAggtttctacCAGATCAccGtaaaTCACTC. actaTCAAGGTGGAATGGCTCGATA
Bacillus halodurans	
NC_002570.1/650317-650406	AATAATCGAAAAACATCATTTTCGtataATGGCAGGAatagg. CCTCGCAGgtttctacCAAGCTAaccGtaaaTAGCTTC. actaCGAAAAATAATGGGTTTTTTAC
Bacillus halodurans	
NC_002570.1/676483-676572	CGTTCTTTATATAAAGTACCTTCAtataATCTTGGGAatatgg. CCCAAAAggtttctacCTGCTGAaccGtaaaTCCGCCG. actaTGGGGAAAGATTTCGATCTT
Bacillus halodurans	
NC_002570.1/806882-806965	TTAATCGAGCTCAACACTCTTCGtata. TCCCTCAtatatgg. GATCAGGgtCtctacAGGTA. . ccGtaaaTACCT. . AGctaCGAAAAAGAATGCCAGTTAATGT
Bacillus halodurans	
NC_002570.1/1593067-1592976	ATTTACATTAAAAAAGCACTCGtataATCCGCCGAatatgg. CCCGCAAggtttctacCAGGCTCccGtaaaCAGCCTC. actaCCAGTCATACTTTCACATAGA
Bacillus halodurans	
NC_000964.1/693955-694038	AGAAATCAATAACATGAATTCGtataATCCGCCGAatatgg. CTCCCAAggtCtctacCAAGCTAaccGtaaaTCCCTTC. actaCCGTAAACATTCTTTCGTTTC
Bacillus subtilis	
NC_000964.1/697886-697976	CATGAAATCAAAACACAGACCTCAataATCTTGGGAatatgg. CCCATPAggtttctacCCGGCAaccGtaaaTTGCCCG. actaTCCAGGAAAGTCATCGATATAA
Bacillus subtilis	
NC_000964.1/2319120-2319031	TTACAATATAAGGAACACTCAataATCCGTCGatatgg. CACCCAGgtttctacCCGGCA. ccGtaaa. TCTCCG. actaTCCGTCAGCAATCGAACCCCA
Bacillus subtilis	
NC_000964.1/4004319-4004410	CATCTTAGAAAAAGACATTTCTTCGtataTCATCAGTAatatgg. TCTGATTgtttctacCTAGTAaccGtaaaAAACTAG. actaCAAGAAAGTTTGAATAAATTT
Bacillus subtilis	
NC_003030.1/1002184-1002270	TATATAAAAACTAAATTTTCGtataC. ACCGGTAatatgg. TCCCGAgtttctacCTGCTC. ccAtaaaa. TAGCAG. actaCCGGGTCGTTATTCATAATATA
Clostridium acetobutylicum	
NC_003030.1/2904259-2904168	GAAAACTAATAACATATTACCCGtataTCCCTTAGAatatgg. TCTAAGCgtCtctacCCGACTCccGtaaaTTGCTC. actaTCCGGTCTTTATAGTATTTTA
Clostridium acetobutylicum	

FIG.41-46A

NC_003030.1/2824539-2824454 AATCGTTAATATAGTTTAACTCATataT. TTCTCGAatatgg. CAGGATgttttctacAAGGAA. ccTtaaa. TTTCTT. actaTCAGTCATTGTGTTGTATGCA
Clostridium acetobutylicum

NC_003366.1/422828-422924 TATGTACTTATATAAGTATATTCGtataTGCCTCGACGatatgg. GTTCAGTgttttctacTAGGAGGccGtaaaCAITCCTA. actaCGAATATATAGGTGATTTCIA
Clostridium perfringens

NC_003366.1/512410-512323 TAAGTGTATTTAAATTTTAACTCGtataTAATTCGTAatatgg. TOCGAAAgtttctctacCTGCTAAccGtaaaATAGCAG. actaCCAGCAGTTCGTACTATATAAAT
Clostridium perfringens

NC_003366.1/2617892-2617807 AAACCGAATATAAACAAACCTCGtataA. GCTTTCGataaagg. CAAGGCGgttttctacCGGAAA. ccTtaaa. TTTCCG. TctaTCAGTCGAATTTCATATATACTAT
Clostridium perfringens

NC_003454.1/1645257-1645173 TAAATAATTTTAATAAAAAATTCGtataA. GCCTAATatatgg. AAGGGTgtCCctacGGTTAA. ccAtaaa. TTAAOCAGctaCGAAAAATGTTTTACTGTGCTT
Fusobacterium nucleatum

NC_002662.1/1159519-1159604 GTCTATAATAGAACAACTCTATTtata. ..CCTAGGatatgg. CTGGCGgttttctacCTCGTA. ccGtaaa. TGCGAG. acaaTAAGGAAATTCGATTTTTTAG
Lactococcus lactis subsp. *lactis*

NC_003210.1/610773-610679 AATCCGCTACAATAATATAGTCGtataAGTTCGTAatatgg. ACCGTTCgttttctctacCAGGCCAaccGtaaaATGCCAG. GctaCGACCTATTTCATAAAATTAAAT
Listeria monocytogenes strain EGD

NC_003210.1/1958601-1958511 ATAACTTAAACCGAAATACTTCGtataATAGTTCGcat. tgg. CCGACCGAgtttctctacCTGCTTAccGtaaaTAACCCG. actaTCAGTCAGTTCGTATAAAGAAG
Listeria monocytogenes strain EGD

NC_004193.1/760480-760571 CAATTTTATCCAATGCTTTTCGtataTCCTCGATAatatgg. TTCGAAAgTAtctctacCCGGTCAccGtaaaTCATCTCG. actaTGAAGGCAGAGCAGGTTCGG
Oceanobacillus iheyensis

NC_004193.1/769695-769781 TGATCTAATTGAATAGAAAATGCGtataATTAAGCGGatatgg. CCGCACAgtttctctacCAGACCAccGtaaaTGGTTTCG. actaCGCAGTAATTATATTGTATC
Oceanobacillus iheyensis

NC_004193.1/786775-786863 CCGACAAATTCGAAAAATGAACCTCATataAATTTCAGAatatgg. CTCAGAAgttttctctacCCAGCA. ccGtaaaTGGCTCGG. actaTCAGCGAAGATGCATCATTTTC
Oceanobacillus iheyensis

NC_004193.1/1103947-1104044 AAACCTTATATATAGTTTTTTCATataATCGCGCGGatatgg. CCTGCAAgtttctctacCGGTTTAccGtaaaTGAACCCG. actaTGCAAAAAGCGGAAAAATTCGAT
Oceanobacillus iheyensis

FIG. 41-46B

NC_002745.1/430771-430861	GTAAATAATTACATAAACCTCATataATCTAAAGaatatggCTTTAGAAgttttctacCATGTTGccTtGaaCGACATG. actaTGAAGTAACAACACAATACTAG
Staphylococcus aureus subsp. aureus	
NC_004461.1/2432384-2432294	CATAAAATAATTATATATGACTCATataATCTAGACaatatggCTTTAGAAgttttctacCGTGTGccataaaCCACACCG. actaTGAAGTAACAATCCAAATACATT
Staphylococcus epidermidis	
NC_004116.1/1093950-1093860	CAATTAAATATATGATTTACTTATTtaT. GCTGAGgat.tgg..CTTAGGgtCtctacAAGACA. ccGt. aa. TGTCTA. acAATAAGTAAGCTAATAATAATAGCT
Streptococcus agalactiae	
NC_002737.1/930757-930842	TGAATTCATAATATGACATACTTATTtaT. GCCTGaat. tgg..CCGACGgtCtctacAAGACA. cc. ttaa. TGTCTA. acAATAAGTAAGCTTTTAGGGCTTGC
Streptococcus pyogenes	
NC_003028.1/1754791-1754878	AAAATTGAATATCGTTTACTTCTTtaT. CTCCTGaat. tgg..CACCAGgtTtctacAAGCTG. cc. Ggaa. CACCT. AacAATAAGTAAGTCACGAGTCAGAT
Streptococcus pneumoniae	
NC_003869.1/586372-586463	AAAAATTTAATAAGACACTCATataATCCGAGaatatgg. CTGGGAggtCtctacCGAACAAccGtaaaTTGTTGG. actaTGAAGTAAGTAAGTCACCTAGCGG
Thermoanaerobacter tengcongensis	
Consensus<<<<<<<<.....>>>>>>>>.....<<<<<<<<.....>>>>>>>>.....>>>>>>>>.....
	*****Y*TWTA*****AT**GG*****GT*YCTAC*****CC****AA*****YWAVR*R****

FIG.41-46C

FIG. 41-47

E. Lysine riboswitch comparison

Command-1 Plain Text

Command-2 Base paired stem 1

Command-3 Base paired stem 2

1. Command-4 Base paired stem 3

Command-5 Base paired stem 4

Command-6 Base paired stem 5

ii. Command-7 Base paired stem 6

Command-8 Terminator poly-U

Command-9 Downstream AI stem paired to stem 1

Command-0 Optional base paired stem 2

cuag is 90% sequence similarity

2. CUAG is the Anti-Terminator

CUAG is the Terminator stem

1. Bha_LysC AGUGAGGUAaggU-gcGAAACC--aG-aguaC-ACAGUCUGAGAGAAUG---AGAUA---CGUUGAC---GACUGUUGGAagg--GGAUUCCgcgaadUGCAGUCCGGG-CUCAUCCC-AUUUGCGUggACCUAUUU---gaaUA-AGCAUAGGgcguucaCAACACUAG-----CCCCAA-----CUAGUGCUUgugagAACUAUCACGU
2. Bha_dapA AGUGAGGUAaggU-gcGAAACC--aG-aguaC-CACAAUUGGA---GGA---GAUUGAGA---UCCGUUGAGAAUUGUG--GAAagg--GGAUUUGccgaagCUGGAGAAU---CUCAU--GUUCUGAAGGCUggUUCUGUAUU---AaaUA-AAUACAGAAcugucaUAUAGCG-----GAUGU-----UGCUAUUAuggagGGcuAUCUCACGC
3. Bha_rhaC AGAUGGGUAaggA-gcGGGUUUU--aG-aguaA-GCGUUG-----GAGGAUGACAACGAGGA-----UAAGCGC-CGAAagg--AAACUCgccgaagCG-GAAGAUG--AGUCAAG-CGUCUUCUUGCUggGGUUGCAUU---gaaUA-AAUGUAACAcugucaCAGC-----AGAUU-----GCUGuggagAACUAACGUU
4. Bsu_LysC GGUGAAGUAaggU-gcGAA-CUUC-aG-aguaU-GCQUUGGAGAA-AGA-----UGGAU-----UCUGUGAA-AAAGCG-UGAAagg-GGAGCGUCCgccgaagCAAAUAAACC--CCAUC-GGUUAUUUUUGCUggCCGUGCAUU---gaaUA-AAUGUAAGGgcguucaAGAA-----UCAU-----UUUUCUuggagGGcuAUCUCGUUG
5. Cac_LysA ACCUUUUGUAaggU-gcUUUAAGUC-aG-aguaA-CCGUUUG--GAGUU-----GGCA-----AACUUAAGUAAGACGG-UAAAgg-GGCUUUUAgcggaagCAUUUAGAUU---GGCA---GAUUUAUUUGCUggCUUUUCAUA---CaaCA-UUAUGAAUGGcugucaCUUUUAUUGU-----AUUAG-GUAAGuggagCGCUACAA--GGU

FIG. 41-48A

6. Cpe_nhaC AAAGA-GGIagaggC-gCGAGAAUC-aAG-auua--CUAAAUGGA---GUU-----AAGU-----AGCGUAGAAGUUUUUAG--GAAagg--
 GAUUAUCgccgaagUUUUUGGCU-AAUACUUUA-GGCUAAAUGCUGGGUGUAUA--gaalUA-UAUACACACugucaCA-----AAA-----
7. Cpe_lysA GACCAAAGIagaggU-gCGUAUU--aAG-agua--GUCAUAAGUAGCUGAC-----AAGU-----GUU--UUAUGUAUAU--GAAagg--
 GAUUAUGgccgaagAGAUUAU--GGUG---AUUAUAUUUUUGGGUUAUAUGUAU---aaU-AUGCAUAUACugucaCUUJ-----GAAA-----
 AAAGuggagUGCUACAAGGUAC
8. Cpe_lysP AACUGAGAUagaggC-gCGAUG-AUU-aU-agua--UUUUUGCAGAGGU-----AAGCA-----AUUGAAGCAAAG-UGAAagg--
 AUGAAUCgccgaAACCAU-UAGAAGAGGUUAUAUUCUAUUAGGUUgGGUUGCAUA--gaalUA-UAUGUAACugucaCAAA-----UUUJ-----
 UUUuggUgUGCUACAUGAAA
9. Eco_lysC CAGGCCAGAgaggC-gCG-U-UGCCCa---aguaACGGUUGUUG---AGGA-----GCCAG-----UCCUGUGUAACACC-----
 UggGGUGCAUCgccgaGUGAUUGAAGG-GCUGGCCA-CGUICA-UCAUCggCUACAGGGG-CUgaalU--CCCCUG-
 GGUugucaCCAGAGCGCUGCAGUGGGCGUUUGCAAGUGggagCACUUCUGGGUGA
10. Htn_nhaC UACAAAAGIagaggC-gcAUUUAU--aUA-agua--UUUUUCAGAG-UG-----GAUAA-----CGAAGAAGAAAAA--GAAagg--
 AAUAGUUgccgaAUCAAAUAAA---GUUG---UUUUGUUGGUUgUGCGUGGUUgC--gaalA-GGG-GCGACACugucaUAGUJ-----UUUCUGAUU-----
 AACUAuggagUGCUACGGUUGU
11. Oth_dapA GUUUUGGAUagaggU-gCGGAGACC--aUC-agua--UAUACGGGA---AGGG---AAUAG--CCCUAGUGAAGCGUAUG--GAAagg--
 GGAUUCgccgaagCGAGU--GAAUACUCAUUA-ACUGGUUgUGGUGCUUAUJ--gaalUA-AAAUACAGUCugucaUAG-----GAGA-----
 CUUAuggagGGCUAUCGAGCUG
12. Oth_nhaC UCGGUGGJagaggA-gcAUAAC--aUU-agua--AUCGAC-----AAGAGGAUGACAACGAUGAUA-----GUUGU--GGAagg--
 GUUGUUgccgaagCA-UAUAAG--GGUICAGA-CUUAUAUUGCUgGUUACAUCUUJ---gaalUA-AAAGAUGCAugucaUGCA-----AAAUUAG-----
 UGCAuggagACUACUUGCA
13. Ptm_nhaC UACUUGUGJagaggA-gcGAUCACU--aUA-agua--UUUUUUGAG-UG-----GAUAA-----CGAAGAGGAAAAAG--GAAagg--
 AGUGACgccgaAUCAAUGAAA---GUCA---UUUUGAUUGGUUgUGGCGUAUUgC--gaalA-GGA-ACGUCAUugucaUAGU-----CUUUUUUA-----
 ACUAuggagCGCUACUUGGUUGG

FIG. 41-48B

14. Sau_1ysC AUUUUUUGAUGaggC-gCAUCA-AUC-aUG-agua--AAGUUUAGA--UUA-----CUGUCUGC-----UAACAGCUGAAUUU--
GAAagg·GUGCGAUGccgaagCGA-UUAUAAU--AGCA-GUUUAUAAUUUGUUGgACUUUUUGGU--UaaGAGCU-GAGAGUUGuCaUUAU--
UAAA-----AAUAUaggagUGCAUCACUUUGUA
15. Sau_1ysP AAUUGAGUUGagaggUUgCAUGUUUA--aUU-agua--ACUUGU-----CAGAAGUAUUUAUGGUACAUAAAGUUAGA--ACAAGU--
GAAagg·UAAAGAUgCcgaaAUAGAUAAU--ACCAUAAA--UUUAUUCUAUUUGgGACAGUUU--CgaaUA-GGAACUGUACugucacA-----GAA-
-----UGUGAugUGcuA-C-CUUUAU
16. Sep_1ysC AGAUUUUGAUGaggC-gCAUCA-AUC-aUG-agua--AACUUUAGAUAAUUUG--UCUGCUAA-----CAA-UUA--UAGAGUU--AAAagg·G-
UGAGAUgCcgaaAUGAUUCAUAAU--AGCA-GUUUAUGAUCGUUGgACUUUAAUUGGU--UaaGAGCUAU-AAAGUUGuCaUUAU--AUUA-----
---AUAUaggagUGCAUCACUUUGUA
17. Sep_1ysP AAUAGAGUUGagaggUUgCAUUAUUA--aUG-aCUa--ACUUAU-----CAGAAGUCUAUGGACAUUGUUGA--AUAAGU--
GAAagg·UAAUAAUgCcgaaAUGAUGUUA-UUU-CCAU-AAAUUAGCAUUUgugGACAAUUU--CgaaUA-GAAGUUGUACuquCaC-----
UUUA-----UGUGAugUGcuA-C-CUUUAU
18. Sf1_1ysC CAGGCCAGAAgaggC-gCG-U-UGCCCa---aguaACGGUGUUGG--AGGA-----GCCAG-----UCCUGUGAUAAACACG---
UGaggGGGUGCAUCgCcgAGUAGUAACG-GCUGGCCA-CGUUCA-UCAUCgGUACAGGGG-CUGaaU--CCCCUG--
GGUUGuCaCCAGAAAGGUUGCGAGUCGGCGUUUCGCAAGUGGuggagCAcuUUCUGGGUGA
19. Son_1ysC AGGAACAGAAgaggA-gcGUUAA-CU-a---Ggua--GUCAAUACAGA---GGAG---CACAAA--CUCAGCGAUUAUGAU--
GAGgg·AGAUUAGCcgCcgagCAUAGAUUG--GUUGCUG-CAUGUUUAUGUGgGUUGCUUAGG-CUgaaU--CCUAACGAUUGuCaCC-----
UGUAUU-----GGuggagAGcuUUCUGGUGAC
20. Son_nhaC CCUUUAAGUagaggC-gCGUGCCU--aUG-aCUa--CUUGUGCG-----GAGGUGAUGCCGCAGA-----UGUACAAG--
GAAagg·AGUCAGCcgCcgaaqUAGC-CAGGU--CAUCA--ACCGAGC-GCUgGUUUUGCAU-CAAUaG--GUGCAAGACugCcaUAGU-----
CAUC-----ACUAUggagCGcuACcUGAAGG
21. Tma_asd GACCCGA-CGaggC-gCGCCCGAG--aUG-agua--GGCUUGUCCC-----AUCAGGGGAGGAUUCG-----GGGACGGGU--
GAAagg·CGAGGGCcgCcgaaqG-GUGCAGAGUUCUCCC-GCUCUGCAUGCCUUGGGGUUUGG--gaaUA-CCCAUACCAcuquCaCGGAGG-----UC--
-----UUCUCCGUGGagAGcCGAUUGGGU
22. Tte_1ysA AGGUGAGGUGagaggC-gcGGGUCAUC-aAG-agua--ACAUGCCAGA--GGU---GUUAAGG-----GCCGAUGAAGGUGUGU--GAAagg-
GGUG-CCCgCcgaaqC-GCGUAAACUU-CCUUAAGGUUUACGCAGCUgagGCCUUAUGCC--gaaCA-GGUUAUAGGACuquCaCUGAAGGU-----CCCCA-----
GGCCUUCAGuggagAGcuAUCUGGCUA

FIG. 41-49A

